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(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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/cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
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Issued\_Patents\_NA:\*

Database :

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US-09-503-922-2	US-08-781-891-209	US-08-473-553A-1	US-07-915-246-1	US-09-228-986-12	US-08-217-327-3	US-07-885-970A-3	US-08-298-687A-3	US-08-530-797-2	US-08-298-829-3	US-08-787-335-2	US-07-885-970A-25	US-08-298-687A-25	US-08-298-829-25	US-08-728-323A-1	US-09-298-568-I	US-08-770-379-20
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## ALIGNMENTS

SULT 1 -09-228-986-4

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
NUMBER OF SEG ID NAS: 1309
SOFTWARE: FastSEQ for Windows Version 3.0 ŝ TTCTCATTACGGGAATTACAGGTTGCAACTGATGGTTTTAGCAATAGAAACATTCTTGGC 1175 AAACGTCTGAAGGAAGAGCGTACACCCGGGTGGAGGTTGCAGTTTCAAACAGAAGTGGAG 1295 1084 GGCGAGGGAC-----GGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGA 1137 1416 GAGAGGECACAAAATGACCCACCCTTAGATTGGCCAACTCGCAAGCGCATAGCATTGGGT 1475 TUTGUTABAGGACTITUTIATUTICATGABGATTGCAATCCTABAATCATTCACCGTGAT 1197 846 964 ATCATCAGCAGAGTICACCACAGGCAICTGGTGTCTTGTTGGTTATTGCATCGCGGT 1023 TICACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGGGAACTTGTTAGGA 947 CAAGGCGGGTTCGGTTACGTGCACAAAAGTGTTGCCTAGTGGGAAAGAAGTTGCTGTG 907 AAGCAGTTGAAAGTTGGGAGTGGTCAG---GGAGAGAGGGGAGTTTCAGGCAGAGGTTGAG 1024 GCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATGTGGAGGTTCACCTCCAT Gaps 15; Length 2868; Score 182; DB 4; Length 28 Pred. No. 8.9e-35; 0; Mismatches 400; Indels ; Sequence 4, Application US/09228986 ; Patent No. 6359198 / Match 9.4%; Local Similarity 52.9%; nes 467; Conservative ( ORGANISM: Pinus radiata 2868 US-09-228-986-4 1236 1138 TYPE: DNA 787 SEQ ID NO 4 Query Match 1116 LENGIH: Best Loca Matches δ g δž d δŏ 임 δ g g δÃ 쉱 ð δ

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Sequence 7, Application US/09228986
Patent No. 6355198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizer, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their USe in the Modification of Plant Cell Signalling
FILE REPERENCE: 11000/1020
CURRENT APPLICANTON NUMBER: US/09/228,986
CURRENT APPLICANTON NUMBER: US/09/228,986
NUMBER OF SEQ ID NOS: 130
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                                                                                                                                                                                                                                                                                                                                                                                                 CIGGTATCGGACAGCGGGAAGGGGCACGTTTCGACGCAAGTGAAAGGCACGCTGGGCTAT 2565
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                                         1027 AAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGGCTTCACCACGCG
                                                                GAGCAGATGTTGGTCTATGAATATATGCCTAACGGGACGCTCAGGGATAGCTTGACAGGA
                                                                                                                         GAGGGACGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCTGCTAAA
                                                                                                                                                                                                         GGACTITCITAICTICAIGAAGAITGCAAICCIAAAAICAITCACCGIGAIAICAAGGUT
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Pred. No. 5.7e-34;
0; Mismatches 274;
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Best Local Similarity
Matches 368; Conserv
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Inches Wodification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION WOMBER: US/09/228,586
CURRENT APPLICATION DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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  1476 TCTGCAAGAGGTCTCCTCCTTGCATGALCATGTGATCCTAAGATTATTCACCGGGAT 1535
                                         1198 ATCAAGSCTTCAAACAIATTGATAGAITICAAGTTTGAAGCTAAGGTTGCTGAITTTGGT 1257
                                                                                                                                                                TTGGCAAAACTIATGGATTATAAGGACACACATGTTACGACGGCTGTTCGTGGAACCATT 1655
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                                                                     CITGCTAAGATIGCTTCTGATACAACACGCATGTATCAACACGTGTGATGGGAACCTTT
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No. 7.4e-35;
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ilarity 55.9%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 2749;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                        AUTHORS: GCRING, DAPHNE
AUTHORS: RCTHSTEIN, SIEVEN J.
TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A
TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES
TITLE: FUNCTIONAL SERINE/THREOMINE KINASE
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749
                                                                                                                                                                                                                                                                                                                                                                                                                  266;
                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 166.4; DB 1.
larity 56.4%; Pred. No. 6.6e-32;
Conservative 0; Mismatches 266
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; Patent No. 6245969
                                                                                                      S-locus
                     Brassica napus
                                                                 Z
                                                                                                                                                      PUBLICATION: I..2574
PUBLICATION INFORMATION:
AUTHORS: GCRING
                                    STRAIN: oleifera
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; GENERAL INFORMATION:
; APPLICANT: Chong, Joane
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 352; Conserv
  ORIGINAL SOURCE:
                     ORGANISM:
STRAIN: ol
                                                                                                                         FEATURE:
NAME/KEY:
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US-08-881-706-1
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                                                                     1430 GCAGCTAGGGGACTGTTATATTGCATGAGCAATGTGATCCCAAGATTATTCACCGGGAT 1489
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                                         1078 CTCCATGGCGAGGGACGGCCTACAATGGAATGCAGCACCAGATTGAAGATTGCTCTTGGA
                                                                                                                           1138 TCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACGTGAT
                                                                                                                                                                                                          1198 ATCAAGGCIICAAACATAIIGAIAGATTCAAGTIIGAAGCIAAGGIIGCEGAITIIIGGI
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APPLICANT: Rothstein, Steven J.
APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
NUMBER OF SECTENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,628
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0 W. Madison St. Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/959,945
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/847,564 FILING DATE: 03-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Pochopien Ph.D., Donald J. REGISTRATION NUMBER: 32,167 TELECOMMULICATION INFORMATICN: TELEPHONE: 312-707-6889 TELEPRAX: 312-707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5821094
GENERAL INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CPERATING SYSTEM:
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CITY: Chicago
STATE: Illinois
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HYPOTHETICAL: N
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US-08-265-628-1
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GEMERAL INFORMATION:
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                                                                                                                                                                                                                                                                               8.4%; Score 162.4; DB 4; Length 4104; 55.4%; Pred. No. 7.9e-31;
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APPLICANT: Li, Jianming
TILE OF INVENTION: Receptor Kinase BINI
FILE REFERENCE: 07251/022001
CURRENT APPLICATION NUMBER: US/08/881,706
CURRENT FILING DATE: 1957-06-24
NUMBER OF SEQ ID NOS: 2
SOFIWARE: PALENTIN VET. 2.0
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Matches 382; Conserv
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                                                                                                                                      LENGTH: 4104
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US-08-881-706-1
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Sequence 9, Application US/07717331F Patent No. 5484905

US-07-717-331E-9

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ACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTTGTCT 1042
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                                                             A Receptor Protein Kimase Gene
Encoded At The Self-Incompatability Locus
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APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 145.6; DB 1;
4.6%; Pred. No. 5.4e-27;
ve. 0; Mismatches 274;
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                                                                                                                                                                     E: Yahwak & Associates
25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/77
FILING DATE: June 19th 1991
                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.6%;
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & 3
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                                                                                                                                                                                                                                                    STATE: Connecticut
                                                          TITLE OF INVENTION:
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                                                                                                                                                                                           STREET: 25 SKy CITY: Trumbull
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1043 ATGAGITTGTTCCTAACAACAATCTCGAGCTTCACCTCCATGGCGA---GGGACGGCCTA 1099
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                                                                                                                                                                                                                                                         1220 TAGATTICAAGIITIGAAGCTAAAGGTTGCTGATTTIGGTCTFGCTAAGA---TTGCTTCTG 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTTGTGCTTT 1396
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                                                                   1802 ATGAGTATTIGGAAAAITTAAGCCTIGAITCTIAICTCTITGGTAAAACCCGAAGGICTA 1861
                                                                                                                                                               1862 AGCTAAATTGGAATGAGAGATTCGACATTACCAAFGGTGTTGCTCGAGGGCTTTTATATC 1921
                                                                                                                                                                                                                                                                                                                                  TIGACAAAAATATGATCCCAAAGATCTCGGATTTTGGGATGGCCAGGATATTTGAAAGGG
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                                                                                                                      CAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                            2042 ACGAAACGGAAGCTAACACAATGAAGGTGGTCGGAACATACGGCTACATGTCCCCGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
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Two Embarcadero Center, Eighth Floor
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17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/567,375
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08587680A Patent No. 5977434 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | || | | || || || || || || || TIGAATISTIAGIGA 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGCTCATTACTGGA 1413
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08
FILING DATE: 07-JUN-1995
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ADDRESSEE: Townsend
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1'
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-587-680A-24
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                                                                                                                    1100
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1277 ATACAAACACGCAFGTATCAACACGTGFGATGGGAACCTFTGGGTACTFGGGTCCGGGAAT 1336
                                                                                       1337 ACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCALTTGGCGTTGTGCTTT 1396
                                                                                                               2102 ACGCAAIGTAIGGGAIATTCTCGGAAAAAICAGATTTTCGATTTTGGAGTCATAGITC 2161
                                           2042 ACGARACGGAAGCTAACACAATGAAGGTGGTCGGAACATACGGCTACATGTCCCCGGAAT 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         983 ACAGGCATCIGGTGTCTCITGTTGGTTATTGCATCGCCGGTGCCAAAAGATIGCTTGTCT 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .682 CGTCAGTTCAAGGGACTGATGAGTTTATGAATGAGGTGACACTAATTGCGAGGCTTCAGC 1741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGTGGTCAGGGAGAGAGGAGTTTCAGGCAGAGGTTGAGATCATCAGCAGAGTTCACC 982
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein TITLE OF INVENTION: A Receptor Protein Kinase Gene TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2833;
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Pred. No. 5.6e-27;
0; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/0717331F Patent No. 5484905
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: George M. Yahwak
REGISTATION NUMBER: 26,824
TELECHMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           1397 TGGAGCTCATTACTGGA 2413
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NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.6'
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy 1
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OPERATING SYSTEM: MG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPCLOGY: 11:
; MOLECULE TYPE:
US-07-717-331F-1
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US-07-717-331F-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCICCAIGGCGAGGGACGCCIACAAIGGAAIGGAGCACCAGAIIGAAGAIIGCICII 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                955 GIGCIICAIGGGAAGAACGGCGGGCAACICCAAIGGGAAACIAGGCIAAAAIAGCCAIA 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GARGCTGCCAAGGCCTTTCTTATTTGCACCACGATTGCTCCCCTATGATAATCCACCGC 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1255 GGTCTTGCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGAT----GGGA 1311
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                                                                                                                                                                                                                                                                                                                                                                        775 CATGEGGGGGAAGAATIGGGAATAAGCAAAGGCECACAIGATAACGGCCTATCEGT
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CORRESPONDENCE ADDRESS: ADDRESSE: TANWAK & ASSOCIATES
STREET: 25 Skytop Drive CITY: Trumbull
                                                                                                                                                                                                                     Length 1554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                Score 140.6; DB 2;
Pred. No. 1.3e-25;
0; Mismatches 274;
REFERENCE/DOCKET NUMBER: 023070-058940US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/07717331F
Patent No. 5484905
            TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA (partial)
                                                                                                                                                                                                                   7.28;
                                                                                                                                                                                                              Query Match
Best Local Similarity 53,44
Matches 318; Conservative
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US-08-587-680A-24
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                                                                                                                                                                                                                                   NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
                                                                                                                                            APPLICATION NUMBER: US/07/7
FILING DATE: June 19th 1991
CLASSIFICATION: 800
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: MICTOSOFT WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                 (203)268-1951
(203)268-1951
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 53.8
Matches 335; Conservative
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US-07-717-331F-4
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06613
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Matches 346; Conservative
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; ORGANISM: Pinus radiata
US-09-228-986-10
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Best Local Similarity
                                                                                                                              US-09-228-986-10
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2336
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 10
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                                          GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Micurehuizen, Miels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1/020
FULE REFERENCE: 11000/1/020
FULE REFERENCE: 1999-01-12
NUMBER OF SEQ ID NOS: 139
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                        GGCTGAAATGCTAGGAAAGGGTAACTTTGGAAGCGCTTATAAGGCTATTATGGAAGATGG 1248
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                                                                                                                                                                                                                                                                                                  Length 2389;
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                                                                                                                                                                                                                                                                                                  DB 4;
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                                                                                                                                                                                                                                                                                                  7.1%; Score 138.2; DB 4 50.9%; Pred. No. 6.4e-25;
                 Sequence 1, Application US/09228986
Patent No. 6359198
                                                                                                                                                                                                                                                                                                                 Local Similarity 50.5 aes 425; Conservative
                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                      2389
09-228-986-1
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Matches
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
COURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
                                                    1953
1539 Teserangacadadadadargecroscargerrecratergecroscerrererratera
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Pred. No. 4.4e-23;
0; Mismatches 337;
                                                                                                                                                                                                                                                                         Sequence 10, Application US/09228986 Patent No. 6359198 GENERAL INFORMATION:
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APPLICANT: Tanksley, Steven D.

PEPLICANT: Marth, Gregory B.

TITLE OF INVENTION: GENE CONFEREING DISEASE RESISTANCE

TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PAT)
1050 TGTTCCTAACAACAATCTCGAGCTTCACCTCCATGGCGAGGGACGGCCTACAATGGAATG 1109
                                                                              1110 GAGCACCAGATIGAAGATIGCICTIGGATCTGCTAAAGGACTTTCTTAICTTCATGAGGA 1169
                                                                                                                                                                    1170 TIGCAATCCIRARATCATTCACCGIGATATCAAGGCTTCAAACATATIGATAGATTTCAA 1229
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                                        348 CATGGAGAATGGGAACCICAAGAGACAITIGIAIGGAICAGAICIACCCACAAIGAGCAI
                                                                                                                  408 GAGCTGGGASCAGAGGCTGGAGAT---ATGCATAGGGGCAGCCAGAGGTCTACAT
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STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/111,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,185
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Patent No. 5648599
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FILING DATE:
RATORNEY/AGENT INFORMATION:
NAME: GOldman Mr., Michael L.
TELECOMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEPHONE: (716)263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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CORRESPONDENCE ADDRESS:
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COUNTRY: U.S.A.
ZIP: 14603
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STRANDEDNESS:
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TO AN AVIRULENCE GENE IN PLANT PATHOGE
           GGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTCTAT 1443
                                    TCTGGTGTCTCTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTTGTCTATGAGTT 1049
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PatentIn Release #1.0, Version #1.25
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50.7%; Pred. No. 7.1e-21;
tive 0; Mismatches 328;
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Tanksley, Steven D.
APPLICANT: Martin, Gregory B.
TITLE OF INVENTION: GENE CONFERRING DISEASE
TITLE OF INVENTION: TO PLANIS BY RESPONDING
                                                                                                                         1684 GAGCGCAIGATTTTAGTGGAGTGGGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/111,078
                                                                                              1444 GTAGATGACAGCTTAGTTGACTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael L.
TELECOMMUNICATION INFORMATION:
TELEPRINE: (716)263-1000
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              Sequence 2, Application US/08447185
Patent No. 5648599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: Floppy disk
IBM PC compatible
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 50.7%
Matches 344; Conservative
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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SOFTWARE: Patenti
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: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14603
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1313 CCTTTGGGTACTTGGCTCCGGAAIACGCTGCAAGCGGAAAGCTCACGGAAAGTCTGACG 1372
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                                                            Length 3097;
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APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
WINMER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                          Score 117.8; DB 4;
Pred. No. 8.5e-20;
0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1493 CTGAGCAAGGAGACTTTGAGGGTTTAG 1519
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Patent No. 6090520
                                                            Query Match 6.1%;
Best Local Similarity 50.4%;
Matches 346; Conservative
       ; ORGANISM: Eucalyptus grandis
US-09-228-986-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
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                                                                                                                              810 AGCCACCAATGGTTTCTCCGAGGCGAACTTGTTAGGACAAGGCGGGTTCGGTTACGTCA
                                                                                                                                                     CAAAGGTGTTGCCTAGTGGGAAAGAAGTTGCTGTGAAGGTTGAAAGTTGGGAGTGG
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                                                                                                 Gaps
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                                                          Length 2443;
                                                                                               Indels
                                                            DB 1;
                                                        Score 121.2; DB 1;
Pred. No. 1.1e-20;
); Mismatches 328;
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Patent No. 6359198
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 DNA (genomic)
                                                    6.2%;
ilarity 50.7%;
Conservative (
                                                                        Similarity
; MOLECULE TYPE:
US-08-447-185-3
                                                                                         344;
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                                                      Query Match
Best Local
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184 TOTOCACCAACTOCATOTACGCCGGGATCTCCACCTCCTTCCTCAGCCGTCTCCACCC 243
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                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Score 117.8; DB 3; Length 7
63.0%; Pred. No. 1.8e-19;
tive 0; Mismatches 107; Indels
                       ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 27-DEC-1996
CLASSIFICATION: 8000
                                                                                                                                                                        ATTORNEY AGENT INPORATION:
NAME: No. 6090520tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/COCKET NUMBER: 39,317
REFERENCE/COCKET NUMBER: 240052.419
TELEPHONE: (206) 62-4900
TELEPHONE: (206) 62-4900
TELEPHONE: (206) 62-6031
INFORMATION FOR SEQ ID NO. 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.09
Matches 182, Conservative
 Washington
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STATE: W
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Search completed: July 7, 2003, 07:26:59 Job time : 119 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

- nucleic search, using sw model OM nucleic

7, 2003, 07:27:14 ; Search time 5106 Seconds (without alignments) 11080.269 Million cell updates/sec July i i

US-10-086-464-1 1944 Perfect score:

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Run

1 atgtcotcggccgtctcc......atagtggaccttctctttaa 1944 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2054640 segs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

GenEmbl:\*

Database

gb\_ba:\*
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gb\_pat:\*
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em\_om: \* em\_or: \* em\_pat:\*

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em\_htgo\_mus:\* em\_htgo\_other:\* em\_htgo\_hum:\* em\_htg\_mam:\* em\_htg\_vrt:\*

em\_htg\_rod:\*

is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AY059901 Arabidops AY093065 Arabidops AX089024 Arabidops AX08882 Sequence AX08888 Sequence AX08888 Sequence AX08888 Sequence AX08888 Sequence AX08888 Sequence AX08888 Sequence AX08889 Sequence AX08887 Sequence AX08887 Sequence AX06977 Arabidops AY05570 Arabidops AY0557 Arabidops AY0557 Arabidops AY08878 Sequence AX08878 Arabidops AY09404 Arabidops AY094451 Arabidops AY094451 Arabidops AY094071 Arabidops AY094071 Arabidops AY094071 Arabidops AY09401071 Arabidops AY094071 Arabidops AY094071 Arabidops AY094071 Arabidops AY094071 Arabidops AY094071 Arabidops AY09408 Arabidops AY094071 Arabidops AY094098 Arabidops AY064968 Arabidops AJ27703 Lea mays AX461250 Sequence AC002330 Arabidops AL161494 Arabidops Arabidops Arabidops Arabidops Arabidops Arabidops Description AX088882 AX088881 AY035076 AC059324 AX088879 AX088878 AY133858 AY091071 AF332429 AY093964 AX088876 AE106957 AX461250 ATCHRIV6 DΒ 70.4 2116
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20.0 2 Length Query 1369.4 1369.4 1369.4 1369.4 1367.8 1341.2 516.2 516.2 446.6 427.2 4427.2 413.6 413.6 405.8 405.8 405.8 402.8 3399.6 39 2215.8 2211.6 2211.6 204.6 204.6 204.6 1195.4 1194.8 1194.8 1194.8 1194.8 Result No. oυ

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 1 AX088876

PAT 17-MAR-2001

linear

DNA

ALIGNMENTS

Sequence 1 from Patent W00114563. AX088876.1 GI:13397639 rape. Brassica napus

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida; II; Brassicales; Brassicaceae; Brassica. [ (bases 1 to 1944) Goring, D. and Silva, N. Proline-rich extensin-like receptor kinases

AUTHORS TITLE REFERENCE

	1021 GGTGCCAAAGGTTGCTTGTCTAAGATTGTTCTAACAACTTCGGGCTTCACCTC 1080 1021 GGTGCCAAAGGTTGCTTGTCTATGTTCTTAACAACATCTCGGGCTTCACCTC 1080 1021 GGTGCCAAAGGATTGCTTGTTGTTCCTAACAACAATCTGAGGTTTGACCTC 1080 1081 CATGGCGAGGGCGCTACAATGGAGGGCCCCAGATTGAAGATTGCTTGGATCT 1140 1111111111111111111111111111111111	AAGGCTTCAAACATATTGATAGATTCAAGTTTGAAGCTAAGGTTGCTGATT	1441   TAIGTAGATGACTTAGTTGACTGGCACGACGACGACGACGACTTGACGAGCATTGACGAGCATTGACGAGCATTGACGAGCATTGACGAGCATTGACGAGCATTGACGAGCATTGATTG
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JOURNAL Patent: WO 0114563-A 1 01-MAR-2C01;  FEATURES  Coring, Daphne (CA); Silva, Nancy (CA)  Location/Qualifiers  1 .1944  Coganism="Brassica napus"  Abarref="taxon:3708"  1 .1944  Codo_start=1  Abarref="taxon:3708"    Abarref="taxon:3708"   Abarref="taxon:3708"    Codo_start=1   Abarref="taxon:3708"   Abarref="taxon:3708"   Codo_start=1   Abarref="taxon:3708"   Abarref="taxon:3708"	Query Match         100.0%;         Score 1544;         DB 6;         Length 1944;           Best Local Similarity 100.0%;         Pred. No. 0;         No. 0;         Additional State of S	TCCT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20   361   CCAICTTCTCCCTCGCCCCGTCTCTTCCGACGGTTATTCAACAGGAGTGGTGGT   420   11111111111111111111111111111111111

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Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (01-JUL-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94364,
                                                                                                                               carried out the
                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members constructed ar sequenced the pUNI (ORF) clones using the RAFL cDNAS: Tripp,M., Kguyen,M., Southwick,B., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Phan,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
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//organism="Arabidopsis thaliana" /db_xref="taxon:3702" /clone="U16568"
                                                                                                                collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKI
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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Enkaryototyta; Magnoliophyta; endicotyledons; core endicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Tripp, M., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Rayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Shinn, P., Yamada, K.,
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PSPPESPRKPPPPPPPRAMSTYFGEFGOOVFGOONASRESDIHVYTSLPP
TNGFSEANLLGQGGFGYVHKGILFSGKEVARVCLKAGSGGGREFQANGILSRA
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YAASGKLITEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLINRASEEGDF
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R. Diect Submission Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                         Collection and clustering of RAFL CDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-Length CDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Edn, C.J., Koesema, E., Meyers, M.C., Shinn, P., Bandh, J. Bowser, L., Dale, J. M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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Location/Qualifiers
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/db_xref="taxon:3702"
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/note="ecotype: Columbia"
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Pred. No. 1.7e-2
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HEDCNPKIIHRDIKASNILLIDFKFEAKVADFGLAKIASDTNTTVSTTWWGTFGYLAPT
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                                                                                                 rne Salx, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                              Nguyen,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers
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/protein_id="AAL24383.1"
/db_xref="G1:16649063"
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Pred. No. 1.7e-265;
0; Mismatches 291;
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                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis
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/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RAFL09-06-A17"
/note="This clone is in
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/gene="MOB24.13"
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32. .1990
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Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA,
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Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Pallin, G.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Rawai, J., Kim, C., Liu, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
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Submitted (22-OCT-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                GAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTTGTG
                                                                                                                   AGUITAGITGACIGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTTGAG
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10   CONTRICTING GRACESTITANCE ARE ARE ASSOCIATED CONTRICTION   1   1   1   1   1   1   1   1   1		1753   GAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGT	AY093065  Arabidopsis thaliana unknown protein (At3q24550) mRNA, complete cds.  AY093065  AY093065  AY093065  AY093065  AY093065  Arabidopsis thaliana.  Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots:  Bosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  Asasa I to 2190)  Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm. G.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Chung,M., Link,G., Lin,J., Liu,S. M., Shida,J., Kamiya,A., Sakano,H., Sakan	Submitted (27-MaR-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA e-mail for correspondence: arab@sequence.stanford.edu the Collection and clustering of RATL CDNAS (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,I., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Faysshizaki,Y. and Shinozaki,K.  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Southwick,A., Nguyen,M., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C., J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
19 TOTCOTTCOTACCANGGATTANCAACAGGAGTGGTGGTGGTGGTATTCAGGAGGGGTGTGTGT			RESULT 6 AY093065 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISN REFERENCE AUTHORS	TITLE JOURNAL COMMENT
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                 Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as Pis. Location/Qualifiers

1. 2190
/ Organism="Marbidopsis thaliana"
/ db.xref="taxon:3702"
/ chromcsome="3"
/ chromcsome="3"
/ clone="RREIO7-12-E08" (R17522)"
/ note="TRIEO7-12-E08" (R17522)"
/ note="This clone is in pBluescript
ecotype: Columbia"
1. 2190
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  and Davis, R.W.
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Pred. No. 1.7e-265;
0; Mismatches 291;
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Best Local Similarity 83.4%;
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ACCESSION

KEYWORDS

SOURCE

VERSION

RESULT 7 AF370509 LOCUS

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

1797

us-10-086-464-1.rge

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LCKKKRRRRHDDEAAYYVPPPPPSGFRAGGPYGGQQYWQQQNASBYDTTTTTPD
PKPPSPPRKPPPPPPPPAFMSSSGSDYSDLPVLPPPSPGLVLGFSKSTFTYEELSRA
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HEDCARKILHRDIRASNILLDRYFERKYADBCLAKIASDTWIHYGTRGYTAPE
YAASGKLITEKSDKSSGVVLLELITGRRPVDANNYVDDSLVDMARPLINRASEEGDF
                                                                                                                                                                                                                                                                                           EGLADSKMGNEYDREEMARWYACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGM
RPGHSNVYSSYGGSIDYDISQYNDDMIKFRKMALGTQEYGTTGEYSNPTSDYGLYPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCCCACCACAC-----CTTCTTCTCTCCCCCCCCATCCACTTTCCGACATCT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGTAAGAAGAAGGACGAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 ACGCGGGATCTCCACCTCTTCCTCAGCGTCTCCACCGGTCCAACTACGCCCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCGTGGTGCCAAAGCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 CACGACGATGAAGCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGA
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Pred. Mo. 3.7e-265;
0; Mismatches 292; Indels
                                                                                                                                                                                                                        /product="protein kinase-like protein"
/protein_id="AAK43886.1"
/db_xref="GI:13877617"
                                                         /note="This clone is in pBluescript
ecotype: Columbia"
1. .2557
/g.ne="MoB4.13"
107. .2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSEGQATREMEMSKIKKTGQGYSGPSL"
                                        /clone="RAFL11-07-N23"
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                                                                                                                                                                          /gene="MOB24.13"
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SCITGOGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGALA 1676
                                                GIGCGIGCGTIAGAAGGAAATGTATCACTGTCAGATCTIAACGAAGGGATGAGACAGGT 1692
                                                                                                                                                              GAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGT 1812
                                                                                                                                                                                                                                                       GAGTACAGTAATCCGACCAGTGACTAJGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGC 1872
                                                                                                                                                                                                                                                                                                                                                                   GAGTACAGTAATCCAACCAGTGACTACGGACTGTACCCGTCTGGTTCAAGCAGTGAAGGT 1916
                                                                                                                                                                                                                                                                                                                                                                                                                 CAAACCACGCGAAAIGGAGAIGGGGAAGAITAAGAGAACCGGICAGGGTIAIAGIGGA 1932
                                                                                                                                         CAAAGCAATGTATACAGCTCATACGGAGGAAGCACGGATTATGACTCGAGCCAGTACAAT 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                         AF370509 2257 bp mRNA linear PLN 30-APR-2001
Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA,
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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CA 94304,
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                                                                     Southwick.A. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosidae, eurosids II Brassicales; Brassicacee, Arabidopsis; Core eurosids II Dases 1 to 2257)
Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, I., Jones, T., Banh, J., Carninci, P., Chenk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stanford, PGBC (SSP) Consortium members carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing and annotation of the RAFL CDNAs: Southwick, B., Karlin-Neumann, G., Mguyen, M., Lam, B., Miranda, M., Palm, C.J., Bbwser, L., Jones, T., Banh, J., Chen, H., Cheny, R., Chung, M.K., Kim, C., Lin, J., Liu, S. X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University, 855 California Avenue, Palo Alto,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e-mail for correspondence: arab@sequence.stanford.edu
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AF370509.1 GI:13877616
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205

90

Gaps

30;

Length 2257;

265

201 325 261 373 321 433 381 493 498

613 555 615

733

674 GGACCITACGGTGGTCACACAGTAITGGCAACAACAAAACGCGTCACGGCCGTCAGAT 616 CATGICGIGACGICACIACCACCACCACCIAAGGCICCATCICCACCACGGCAACCICCI

g

12257 /organism="Arabidopsis thaliana" /db\_xref="taxon:3702"

source

FEATURES

673

675

Query Match Best Local Similarity 82.8%; Pred	1893 CAAAGCRAIGTATACAGCTCATACGGAGGAAGCACGGTTATGACTCGAGCCAGTACAAT 1752 	Ž a
/OLGALINE-MADIOC /OLGALINE-MADIOC /OLGALINE-MADIOC BASE COUNT 583 a 566 c 483 g	1633 GTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGGATGAGACCAGGT 1692 	Qy Dp
FEATURES 1. 2324  Source 12324	1573 GCTTGTGCTGCGGGTTGTGTTCGCCATTCAGCTCGCGCAGACCTCGCATGAGCCAGATT 1632 [HII] [H	Qy
C-terminal end or the encox sequences are derived from may contain polymorphisms of Genset Carried out the liby	1513 GGTTTAGCTGATGCAAGATGATAATGGGTATGACAGAGAGGAGATGGCTCGCATGGTT 1572 	da Db
percent may contain premate frame shifts in a coding restricted if it lacks the sequence is considered to lead	1453 AGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTTGAG 1512 	Oy Op
the clones are estimated the clones are estimated that are 3'-truncated; approximately splice variants, including	1393 CTTTGGAGCTCAFTACTGGACGTCGATGATGCCAACAATGICTATGTAGATGAC 1452 	da da
COMMENT This clone sequence is one available to TIGR and Genb	m <del>st</del>	QY Db
	1273 TCTGATACAAC&CGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGGTCCG 1332	ga Ga
Brover, V., 7 Feldmann, K. Full-Length Unpublished	1213 ATAITGATAGATTCAAGITIGAAGCTAAGGITGCIGAITTTGGICITGCIAAGATTGCT 1272 	ÅÖ qa
TITLE FULL-length messenger RNA annotation JOURNAL Genome Biol. (2002) In pre REFERENCE 2 (bases 1 to 2324)	1153 TCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATCAAGGCTTCAAAC 1212 	Qy Bb
CE RS	1093 CGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCTGGTAAAGGACTT 1152 	Qy Dp
SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Spermatophyta; Magnoliophy	1033 TIGCTIGICATGAGTITGITCCTAACAACAATCTCGAGCTICACCTCCATGGCGAGGA 1092 11	QY Dp
DEFINITION Arabidopsis thaliana clone ACCESSION AY089024 VERSION AY089024.1 GI:21407798 KEYWORDS FLI_CDNR.	973 AGAGTICACCACAGGCALCIGGTGTCTCTTGTTGCTTATTGCALGGCGGTGCCAAAAGA 1032 	da D
AY089024	913 TTGAAAGTTGGGAGZGGTCAGGGAGAGGAGGGAGGCAGAGGTAGAGATCATCAGC 972 	QV.
Oy 1933 CCTTCTCTTAA 1944  Db 2054 CCCTCTCTTAA 2065	853 GGGTTGGGTTACCTGCAAAGGTGTGTTGCCTAGTGGGAAAGAAGTTGCTGAAGCAG 912 	QY DP
QY 1873 CAACCACACGGAAATGAATG 	793 TACGAGGACTAGACTAGACCACCAATGGTTTCTCCGAGGCGAACTTGTTAGGACAAGGC 852 	QQ AG
Oy 1813 GAGTACAGTAATCCGACCAGTGAC	733 CCAGITCIICCTCCACCGICTCCAGGGCITGTGTTAGGCTTCTCCAAAAGCACITTCACA 792 	čč GD
OY 1753 GAAGACATGAGAAGTTTAGGAAA	676CCACCICCACCACCCCTTTCAIGAGCAGCACGCGCTCCGACTACTCGAACGT 732	QY
( L C	≠df	qa

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Genbank. The following quality assessment of comparison with known proteins: two percent of ted to be 5-truncated; less than one percent oximately two percent represent alternative ding unspliced infroms and spliced exons; one remature stop codons; five percent may have my region. A sequence is considered to be my region. A sequence is considered to be its the translation initiation start (ATG). A lito be 3'truncated if it lacks the encoded protein. Please note that these cDNA from the Ws or Laker ecotypes and therefore sime when compared to sequences from Col-0. These, Inc. carried out the clustering of the not clones, and sequence assembly.
                                                                                                       ACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGC 1872
                                                                                                                                                                                                                 AAATGGCACTTGGAACTCAAGAGTACAACGCCAGGGGT 1812
                                                                                                                                      1324 bp mRNA linear PLN 21-JUN-2002 ie 17909 mRNA, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots; issicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Town, C.D., Troukhan, M., Alexandrov, N., B., White, C. and Salzberg, S.L., sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mexandrov, N., Lu, Y. -P., Flavell, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lexandrov, N., Lu, Y.-P., Flavell, R. and
                                  AAATGGTTTTGGAACTCAAGAATACGGCACAACCGGC
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AXO88881 1539 bp
Sequence 6 from Patent WO0114563.
AXO88881
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QOSTGGWGGGGOEPPPPRHPSGEDSSMYSGPRSPYLPPPSPALALGFRKSFFYOD
LAAATGGFTDANLLGGGGFGYVHKGVLP SGKEVAVKSLKAGSGGGREFQAFUTISR
VHHRYLYSLVGYCLADAOGAMLYYEFVPHKTLEYHLEGKNLPYMEFSTRLRIAGAAKG
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LAPEYASSGRILTEKSDYFSTYGVMLLATTGRRFYDNSTHODTLVDMARTEGY
GNENBILADARLEGGYRYRQEMARWYCCAASTRHSGRRFKMSQIYRALGGTSGYSDAL
EGYKPGHSNYYGSLGASSDYSQTSYNADMKKFRQIALSSQEFPVSDCEGTSSNDSRDM
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 1.1e-93;
0; Mismatches 363; Indels 3;
             1 (bases 1 to 1962)
Goring, D. and Silva, N.
Proline-rich extensin-like receptor kinases.
Patent: W0 0114563-A 7 01-MAR-2001;
Goring, Daphne (CA); Silva, Nancy (CA)
Location/Qualifiers
                                                                                                      /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae, eurosidas II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1939;
Goring.D. and Silva,N.
Proline-rich extensin-like receptor kinases
Patent: WO 0114563-A 6 01-MAR-2001;
Caring. Daphne (CA); Silva, Nancy (CA)
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                       1417 AIGTTATTGGAACTTATAACTGGAAAACGACCGGTTGAT---AATAGCATCACCATGGAC
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                                                                                                GIGCTITIGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTCTATAGAT
                                                                                                                                                                                                GACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTT
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Pred. No. 1.1e-93;
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                                  1014 AGCCGTGTGCATCATCGTATCTTGTTTTTTTGGTTGGATATTGCTAGACAGGACAG
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            GGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTTGCTGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                               CTITCITATCITCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATCAAGGCTTCA
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                                                                                      CAGTTGAAAGTTGGGAGTGGTCAGGGAGGAGGGAGTTTTCAGGCAGAGGTTGAGATCATC
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Institute, Department of Plaint Gene Research; 1532.3, Kana, Kisaraau, Chiba 222-0812, Japan (E-mail:ynakamuekazusa.or.jp, Tel:81-438-52-3934)

Address for correspondence: Kaosékazusa.or.jp
Ror the latest information on amotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MoB24 Genes with similarity to proteins in the databases are described in protein similarity or proteins in the databases are described in protein similarity are described as 'unknown protein.'

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, Http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), MetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://compin.org/lastate.edu/cgi-bin/sp.cgi).
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4757. .5179,5354. .5548,5693. .5970,6088. .6214,6297. .6496,
6601. .6648,6743. .6776,6882. .7013,7464. .7559,7677. .7743,
8162. .8217,8290. .8385,8470. .8998,9122. .9462))
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl. TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wnstl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
The 5' clone is MXP5 and the 3' clone is MSD24.
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VEGEEEDPQGGYIRGNERFQKRQKPNKVYSGFEFAGPSDAKVAYDWREQEAFVLLEVW
GDRFLQLGRRSLRNEDWNEVAEKVSEELRMEKSETQCRRMIDDLKRKYRKEKIKVEKS
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ADFGRDLELQKKQIVDRAQSELARLREEEENHHGGGDDDESEDEEMENDSDVNLSDE"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Direct Submission
Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone: MOB24.
AB020746 BA000014
AB0207461 GI:3985949
                                                                                                                                                               Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                      Spermātophyta; Magnoliophyta; ēudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/organism="Arabidopsis
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2398. .3399
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unknown protein"
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DNA Res. 7 (3), 217-221 (2000)
20363099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                     clone:MOB24.
Arabidopsis thaliana
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38288. 38398, 38486. 38584, 38662. 38772, 39019. 39066,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PEVLAQTOMKLEMNONEDARSIRGEFENSVLEETSMAESIVVLDSDDSGQEREERVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSSLIAYLSEFSNESPLEKLSRILSNEWLLYRTSTNIKRKRWCL
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TNHNELVLIWLHKNSLRTLPLVSSRTFVTGFICLKNNGIMPPTPTSFWCDLCHPSATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CISPTHLGISFKQSCISSRVKAHISRISKEVPNLFEIITBPSPHALVVKGLKKIBINI
SPRSGDYQFRPNLSHSYPLTTEKFKQKRNIIKTSHDLGISCHKGHMISSPWSDDYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(32831, .33058,33143, .33907)
/note="contains similarity to heat shock transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGICCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCAT-----CA
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       /note="contains similarity to ubiquitin conjugating
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Pred. No. 1.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28636. .30168
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66.28;
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Best Local Similarity
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13623. 13765,14306. 144405);
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/db_xrei="C1:9294040"
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/protein_id="BAB01998.1"
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UDDKRTNGGNNNRDGSTPSPPSGNRTSGDGGSP
LANCICICCNERKKKRSPQWHMHYYNNNPYGGA
SOWGEODPWSGPSDASNIGERTJERPQATLG
GGGEGTWHKGVLPSGKEYWYKSLKJGSGGERE
SGGGRLLVYEPIPNTLEFFILDFSPWTDPPT
HICLISHENIHMEDIKANILLDFSPSTWADDFGL
BYASSGKLSNKSDYFSFGWLLEITTGRPPLDLT
NQLADPRLEINYSHQEWYQMASCAAAAIRHSARR
EDMSMDDLSEGTRPGGSYYLSFGSWSSEYDASSYT
SEGGLNPSASSSEEMNRGSMKRNPQL\* PAT 17-MAR-2001 4. ATCGCCGCTGCCAAAGATTGCTTGT 1040 yta; Embryophyta; Tracheophyta; octyledons; core eudicots; Brassicaceae; Arabidopsis, CACCTCCATGGCGAGGGACGGCCTAC 1100 800 CTCCGACTACTCGGACCGTCCAGTTCT 740 SAACTTGTTAGGACAAGGCGGGTTCGG 860 917 AGAAGTTGCTGTGAAGCAGTTGAAAGT 920 573 CTCCAAAAGCACTTTCACATACGAGGA DB 6; Length 2025; e-76; 413; Indels 75; Gaps linear kinases liana" duct" ; (CA) DNA a

Arabidopsis.

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Rosidae; eurosids II; Brassicales; Brassicae 1 (bases 1 to 2104)
Goring,D. and Silva,N.
Prolline-rich extensin-like receptor kinases Patent: W0 0114563-A 9 01-MAR-2001;
Goring, Daphne (CA); Silva, Nancy (CA)

REFERENCE AUTHORS JOURNAL PEATURES

1. .2104 /organism="Arabidopsis thaliana" /db\_xref="taxon:3702"

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PAT 17-MAR-2001

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DNA

AX088884 2104 bp Sequence 9 from Patent W00114563

DEFINITION

RESULT 13 AX088884 LOCUS ACCESSION VERSION KEYWORDS SOURCE

GI:13397647

Arabidopsis thaliana

ORGANISM

thale cress. AX088884.1

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Match 21.3%; Score	Similarity 67.0%; Pred. No. 5e-73; 6; Conservative 0; Mismatches 289; Indels GCACTITCACATACGAGGAGCIAGCTAGAGCCACCAATGGTTTCICC		QY 842 TAGGACAAGGCGGGTTCGGTTACGTGCCAAAGGTGTTGCCTAGTGGGAAAGATGT 901	902 CIGTGAAGCAGTIGAAAGTIGGGAGTGGTCAGGGAAGAGGGAGTTTCAGGCAGAGGTTG 9	Db 1244 CGGTGAAGCTGAAGATTGGGACTATCAAGGGGAAGAATTGCAAGCTGAGGTTG 1303  QY 962 AGATCATCACAGAAGTTCACACAGGCATCTGGTGTTGTTGCATGCCG 1021	Db 1304 ACACAAACAGTAGGTTCATCAACACTTCATTGTTTTTTTT	TGC 14	OY 1082 ATGGGGGGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGGATCTG 1141	OY 1142 CTPARGGACTTTCTTATCTTCAGGAGATTGCAAAATCATAGACGTGATATCA 1201	OY 1202 AGGCTTCAAACAIAIGATAGATTCAAGITTGAAGGTGCTGAGGTTTTGGTCTTG 1261   1   1   1   1   1   1   1   1   1	OY 1262 CTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGAA 1312 	Qy 1313 CCITTGGGTACTEGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACG 1372	QY 1373 TTTCFCAFTFGGGTTGTTTFGGAGCTCATTACTGGACGTGGACCGTTGAFGCCA 1432   1   1   1   1   1   1   1   1   1			Db 1844 TCTCTGGAGAAAGTTTTGACTTGTTGAGACTCAAGGTTGGAGAAGTACGATACAA 1903  Qy 1553 AGGAGATGGCTGGCTTGTGTGTGCTTGTGTTGGCCGCATTCAGCTCGCCGA 1612	1904 CTCAGAIGGCAAACAIGGCIGCTGCTGCTTGCATACGCCAATCAGCTTGGCTTC 196	QY 1613 GACCTCGCATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTA 1672	1673	Db 2024 AAGA 2027	RESULT 15 AX088887	
OY 1488 AGCACCTGAGCAAGGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGA 1547	1514 MCGGGICGGGAGGIGGGGGGGGGGGGGGGGGGGGGGGGGG	1608 CCGCAGCACGCATGAGCCAG	1 15		QY 1695 AAGCAATGTATACAGCTCATACGGAGGAACCACGATTATGACTCGAGCCAGTACAATGA 1754	OY 1755 ACACATGAAGAATTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGTGA 1814	OY 1815 GTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAACGGGGGCCA 1874	Db 1967AatatGGTGAACAGTGAGTTAAACCCTTCTGCTTCAAGTAGTGAAAT 2024 Qy 1875 AACCACACGCGAAATGGA 1892	2025	RESJIT 14 AXO8888 LOCUS BEFINITION Sequence 13 from Patent WO0114563.	ACCESSION AX088888 VERSION AX088888.1 GI:13397651 SETWORDS thate cress.	ENESM ALE EUK Spe Ros	- 있는 본조	e G	/organism="Arabidopsis thaliana" //db.xref="taxon:3702" L. 2196 /note="unnamed protein product"	/codon_start=1 /protein_id=~cAC34707.1" /db_xref="GT:13397622"	/translation="MSLSPSSSPAPATSPPAMSLPPADSVPDTSSPPAPPLSPPL SSPPPPLSAPTASPPLPVESPPSPHY SSPPPLLESPPPEPSPHY SSPPPLSAPTASPPLPVESPPSPHY	SAPSGEFELFELFAKPSFPESSFPETY PFGATISFPFASLFDESTFFYNIABEFFF5 PPRRASCPRESCPPPINSSPPNPSPMTPSLFPTSPPFKAFFFSSTPPPKKSP AAVTLEFFGPAQLPDGTVAPPIGPVIEFKTSPESTSPGTPQPLVFKLSFHR SSAGFFFGGALTLEITGILFGTFFYFYFATRRNNGSSAHGOSKTPEKVGHRGGNA	GINGART TIMPPPIHAKY ISSGGCDTKENNSVAKNI SMPSGMFSYEELSKATGGFSEE GINGART TIMPPPIHAKY ISSGGCDTKENNSVAKNI SMPSGMFSYEELSKATGGFSEE NLLGEGGFGY VHKGVLKNGTEVAVKQIK ISSGGGERDE SANNAN SKAT SKETTING CHI	YCVNGDKRLLVYEFVFKDTLEFHLHENRGSVLEWEMRLKIAVGAAKGLAILHENCSPT IIHRDIKAANILLDSKEFAKVSDFGLAKFFSDINSSFHISTRVGTFGEWAPEXASS GKVTDKSDVYSFGVVLLEI ITGERS IFAKDSSTNOSUVDWARPLLITKAISGESFDFLV	DSRLEKNYDTTQMANMAACAAACIRQSAWLRPRWSQVVAALEGEVALKKVEETGNSVT YSSSENPNDIIFRYGTNKRRPDIGSSOGYTSEYGVNPSQSSSEHQQVNI" BASE COUNT 546 a 637 c 446 g 567 t	

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                                                                thale cress.

Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Eukaryota;
Spermatopiyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 2261)
Goring.D. and Silva,N.
Proline-rich extensin-like receptor Xinases
Patent: WO 0114653-R 12 01-MAR-2001;
Goring.Daphne (CA); Silva, Nancy (CA)
Location/Qualifiers
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I7-MAR-2001
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Pred. No. 5e-73;
0; Mismatches 289;
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/db_xref="taxon:3702"
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WO0114563.
            Sequence 12 from Patent
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                                            AX088887.1 GI:13397650
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al Similarity 67.0%;
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Search completed: July 7, 2003, 09:38:57 Job time : 5136 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July Run on:

7, 2003, 06:45:11; Search time 465 Seconds (without alignments) 9414.806 Million cell updates/sec

US-10-086-464-1 1944 Perfect score:

1 aigrecteggegegegtetec.....atagtggacettetetttaa 1944 Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

2i85239 seqs, 1125999159 residues Searched:

4370478 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		Description			pressica napus PER	Arabidopsis thalia	Zea mays DNB fragm	Arabidoneis +halia	Park and Colored	Alabinopsis Inalia	Arabidopsis thalia	Arabidopsis thalia	Arabidoneia the 1:-	PITELIA STEAMING TO THE TIE	Arabidopsis thalia
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## ALIGNMENTS

RESULT 1

AAF77094 standard; DNA; 1944 BP. (first entry) Brassica napus PERK1 DNA. 17-MAY-2001 AAF77094; 

Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.

Brassica napus.

WO200114563-A1.

18-AUG-2000; 2000WO-CA00966. 01-MAR-2001.

99US-0149466. 99US-0159122. 19-AUG-1999; 13-OCT-1999;

(GORI/) GORING D. (SILV/) SILVA N.

Goring D, Silva N;

WPI; 2001-244305/25.

New proline-rich, extensin-like receptor kinase nucleic acids and

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polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding
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1861 AGCAGGGGCCAAACCACACGCAAATGGAGATGAGGAGATAAGAGAACCGGTCAG 1920
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protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.
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    TIGATAGATTICAAGITTGAAGCTAAGGITGCIGATTTTGGTCTTGCTAAGAITGCTTCT 1275
                                                            GAZACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCTCCGGAA 1335
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1006 GGTTATIGCATCGCCGGTGCCAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAAAA 1065 946 TITCAGGCAGAGGIIGAGAICAICAGCAGAGIICACCACAGGCAICIGGIGICICITGII 1005 1120 ITGAAGAITGCTCTTGGATCTGCTAAAGGACFTTCTTATCTTCATGAAGATTGCAATCCT 1179 769 GGCTTCTCCAAAAGCACTTTCACATACGAGGTAGCTAGAGCCACCAATGGTTTCTCC 209 GCCAICICAGGGGAACIIICACCIICGGGGGGCTGGCTACGGCCACCAGGAACIICAGG 569 ATGARARTTGCAGCAGGTGCTGCCARAGGACTGGAGTACCTTCATGACAAAGCTAATCCA 886 AGTGGGAAAGAAGTTGCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGGG 12; Gaps DB 21; Length 1703; Indels Score 215.8; DB 21; Pred. No. 1.6e-41; 0; Mismatches 287; 9905-0155139.
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                             1297 ACACGIGIGAIGGGAACCITIGGGIACTIGGCICCGGAAIACGTGCAAGGGGAAAGCIC 1356
                                                                                                                                                          1417 CGACCCGTTGATGCCAACAATGTCTATGATGACAGCTTAGTTGACTGGGCACGACCA 1476
869 AGGGTATTGACAGCACCAGACCACATGGAAAATCTTGTCTCATGGGCACGTCT 928
                                                                                  1357 ACGGAGAAGTOTGACGTTTTCTCATTTGGCGTTGTGCTTTTGGAGGTCATTACTGGACGT
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                                                                                                                                 0; Mismatches 289;
                                                                                                       Score 204.6; DB 2
Pred. No. 6.9e-39;
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990S-0161359.
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                                                                                                   Query Match 10.55
Best Local Similarity 57.25
Matches 394; Conservative
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metabolic pathway; promoter; termination sequence; ss
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ATAITGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTTGCTAAGATTGCT 1272
                                                                                                                                                          TCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCTCCG 1332
                                                                                                                                                                                                                                     GAATACGCTGCAAGCGGAAAGCTCACGSAGAAGTCTGACGTTTTCTCATTTGGCGTTGTG 1392
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                                                                                                                                                                                                                                                                                                                                                    1054 ATCATGGAGATAATCACCGGAAGAATCCTGTCGATTATAGTCGACCTCAAGGAGGTG 1113
       1153 TCTTAICTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATCAAGGCTTCAAAC 1212
                                             873
                                                                                                                                                                                934 TTCTCCGAGAGCAGCTACGTGACAACCCGAGTAATGGGAACTTTTGGATATGTTGCGCCT 993
                                                                                                                                                                                                                                                                                                                                                                                        1453 AGCTTAGTTGACTGGGCACGACCATTGCTT----AACCGAGCATCTGAGCAAGGAGAC 1506
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990X-0153758.
990X-0154018.
990X-015473.
990X-0155486.
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Matches 408; Conservative
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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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    GCTAAAGGACTITCITATCTICATGAAGATTGCAATCCTAAAATCAITCACCGTGAIATC 1200
                                                                                        1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260
                                                                                                                                                                         1281 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320
                                                                                                                                                                                                         TACTIGGCICCGGAATACGCIGCAAGCGGAAAGCICACGGAGAAGICIGACGIIIICICA 1380
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                                                                                                                           919 AAGTCAAGCAACAITCIGAICAAIGAGAAITCAACGCAAGGIITCAGAITIIIIII III
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Best Local Simil
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PRANTON NEW YORK NAME OF PRANTON NEW YORK NAME

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1180 AGACCGCCTGGCGAGATGAACTTAGTGGATTGGTTCAAAGGAATGGTTGCAAGTAGACGT 1239
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940 GAIGTGAAAICTAGTAACAICTIGCICGAIAAGAAAIGGAACGCGAAAGIGICTGAITIT 999
                         GGTCTTGCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACC
                                         1000 GGTTTGGCCAAGTTATTAGGATCTGAAAGCTACGTGACACTGGCTGACTGGTGATGGGAACT
                                                                          TITGGGTACTIGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTT
                                                                                                                           TTCTCATTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAAC
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protein identification; signal transduction patkway;
metabolic pathway; promoter; termination sequence: ss.
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99US-0123180.
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99US-0125788.
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990S-0160768.
990S-0160770.
990S-0160814.
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99US-0158369.
99US-0159293.
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990S-0160981.
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99US-0161361.
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04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
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12-0CT-1999;
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990x-0145951. 990x-0146386. 990x-0146389. 990x-0147038. 990x-0147302. 990x-0147302. 990x-0147303. 990x-0147416.	990x-0147935. 990x-0148171. 990x-0148341. 990x-0148565. 990x-01493684. 990x-0149175. 990x-0149175. 990x-0149920. 990x-0149902. 990x-0149902. 990x-0149902. 990x-015066.	990x-0151303 990x-0151438 990x-0152363 990x-0153070 990x-0154018 990x-0154018 990x-0154039 990x-0155139 990x-0155486 990x-0155486 990x-015569 990x-0156458 990x-0156458	990x-0158369. 990x-0158289. 990x-0159293. 990x-0159295. 990x-0159331. 990x-0159631. 990x-0169631. 990x-0160741. 990x-0160741. 990x-0160781. 990x-0160814. 990x-0160814. 990x-0160814. 990x-0160818.
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990S-0134941. 990S-0135124. 990S-0135523. 990S-0136629. 990S-0136629. 990S-0136782. 990S-0137722. 990S-0137724.	99US-0138540. 99US-0138847. 99US-0139452. 99US-0139453. 99US-0139455. 99US-0139456. 99US-0139456. 99US-0139456. 99US-0139456. 99US-0139456. 99US-0139461. 99US-0139461. 99US-0139461.	990S-0145999. 990S-0140353. 990S-0140354. 990S-0140695. 990S-0140691. 990S-0141287. 990S-0142187. 990S-0142187. 990S-0142187. 990S-0142187. 990S-0142187. 990S-0142187. 990S-0142187.	990S-0144331. 990S-0144333. 990S-0144333. 990S-0144334. 990S-0144352. 990S-0144884. 990S-0144884. 990S-0145086. 990S-0145086. 990S-0145087. 990S-0145087. 990S-0145192. 990S-0145192. 990S-0145192. 990S-014518.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-0131449.
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                                                         Arabidopsis thaliana
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        CACCACAGGCATCTGGTGTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTT 1038
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                                                                                                           799 GAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTGTTAGGACAAGAGGGGGGTTC
                                                                                                                                                                                                       450 GAGCTTGAGGTTTCTACTAATGGATTTGCTGACGAGAATGTGATTGGACAAGGAGGTTAT
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                                                                         DB 21; Length 1479;
                                                                                             Indels
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                                                                       Score 194.8; DB 21;
Pred. No. 1.5e-36;
); Mismatches 312;
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990S-0161992.
990S-0161993.
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                                                                                                                                                                                                                                 GTCAAAAGCAAGGCAGAATCTTGTTACTTGGTCACGTCCATACCTCAAGGATCAGA 1272
                   912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bucalyptus grandis; Pinus radiata; Wonterey pine; plant; modification;
plant cell signalling; modulation; transgenic plant; pathogen; growth;
environmental change; development; cell proliferation; differentiation;
elongation; survival; disease resistance; nutrient metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diated polynucleotide encoding a polypeptide involved in cell gnaling used for generating transgenic plants with modified responses external signals -
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TGATCTTGAGTCTAATCAAGAACCATTAAGCTGGAATACTGGAATGAGAAATCGGGGTTG
                                        GATCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTG
                                                                   GIGCAGCTCGAGGAATAGAGTATCTTCACTGCACAGCTAACCCGCCAGTGATTTACCGTG
                                                                                                                        ATTIGAAATCCGCAAACATATTGTTAGATAAAGAGTTCAGTCCAAAACTCTCGGATTTCG
                                                                                                                                                                                  GATTGGCGAAACTCGGTCCAGTTGGTGATCGAACTCATGTATCGACTCGTGTCATGGGAA
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                                                                                                                                                                                                                                                                      TITICICALITIGECSITGICTITIGGAGCICATIACIGGACGICGACCCGIIGAIGCCA
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are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differantiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or senescence providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear valuable knot-free clear valuable knot free clear valuable knot free clear valuable knot senescence.
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0; Mismatches 356;
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                                                                                             Proline-rich extensin-like receptor kinase; PERK; resistance;
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Pred. No. 8.2e-36;
               AAF77097 standard; DNA; 2820 BP.
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                                                                                                                           Arabidopsis thaliana.
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CCACAGGCATUTGGTGTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTTGT
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Pred. No. 8.8e-36;
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  1082 AGCCGTGTGCATCGGTATCTTGTTTGGTTGGATATTGCATAGCTGATGGACAG 1140
961 GGAGGAITIGGGTATGTCCATAAAGGAGTCTTGCCTAGCGGGAAAGAAGTAGCAGTTAAG 1020
                        970 AGCAGAGIICACCACAGGCAICIGGGGICICITGIIGGIIAIIGCAICGCGGGGGCCAAA 1029
               910 CAGTIGAAAGTIGGGAGTGGTCAGGGAGAGGGAGTTTCAGGCAGAGGTTGAGATCATC
                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 65175.
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'n 1000 1015 1016 TCGCCGGTGCCAAAAGATTGCTTGTCTAIGAGTTTGTTCCTAACAACAATCTCGAGCTTC 1075 1180 703 718 CTCTTGGATCTGCTAAAGGACTTTCTTATTGAAGATTGCAATCCTAAAATCATTC 1189 1190 acceterateargetteaaacatattgatagatticaagtttgaagetaaggtigetg 1249 764 AGGACCACTITITGALGIACCIGCIGAAGAGCCCAGAGGIICATTIAGGACAACICA 823 838 1310 GAACCITTGGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTG 1369 AAAG---GITTACCTTGCGTGAACTGTTAGTTGCTACTGATAACTTTAGCAATAAAATG 880 599 CAACACCACGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTC 659 CACCACGGCAACCTCCTCCACCTCCACCCTTTCATGAGCAGCAGCGGCGCTCCG AAAGCACTITCACAIACGAGGAGCIAGCIAGAGCCACCAAIGGITTCICCGAGGCGAACT ACTACTCGGACCGTCCAGTTCTTCCTCCACGTCTCCAGGGCTTGTGTTAGGCTTCTCCA 941 TGGCTGTCAAAAGGCTAAAAGAAGAACGTACCAAGGGTGGGGAACTGCAGTTTCAAACCG 839 TGTTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTTGCCTAGTGGGAAAGAAG TTGCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAG---GGAGTTTCAGGCAG 956 AGGTTGAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTATTGCA 1061 reactccaactgaagarractrgrrrancccracarggcraarggaagrgrrgcrrcrr 1250 ATTTIGGTCTTGCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGG 12; 1370 ACGITITCICATITGGCGITGTGCTTITGGAGCTCATIACTGGAC 1414 Indels Pred. No. 8.7e-36; 0; Mismatches 362; 54.78; 451; Conservative Best Local Similarity Matches 451; Conserv 950 719 179 824 1130 1241 ద ŏ 임 ð 絽 ŏ 쉽 ð g ŏ d δã g δλ q ð g ö g ŏ a g ð å ò õ d

Search completed: July 7, 2003, 08:13:00 Job time :  $480~{\rm secs}$ 

Query Match

DB 21; Length 1848; Score 191.8; 9.98;

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1270	US-09-938-842A-1270	σ	2640	;; œ	158.2	41
Sequence 1495, Ap	US-09-938-842A-1496	on	2532		158.4	40
414,	US-10-101-464A-414	σ	758		159	39
Sequence 888, App	US-10-101-464A-888	σ	4356	8.5	160.2	38
340, A	US-09-938-842A-340	თ	1389		161.4	37
1750	US-09-938-8428-1750	σ	1902	e, e	161.6	36
87	US-10-101-464A-874	σ	2315	8,3	162.2	35
1, Apr	US-09-823-394-1	σ	4104	8.4	162.4	34
1479,	US-09-938-842A-1479	σ	3012	8.4	163	33
1181,	US-09-938-842A-1181	σ	3591	8.4	164	32
2569	US-09-938-842A-2569	σ	2493	8.5	166	31
57, Ap	US-09-938-842A-57	σ	2631	8.6	157.6	30
2362	US-09-938-842A-2362	σ	1977	8.6	1.58	29
461, A	US-10-101-464A-461	σ	2175	8.7	168.2	28
65	US-09-887-576-654	10	2448	8.7	170	27
	US-09-938-842A-51	σ	2448	8.7	170	26
799	US-09-938-842A-799	σ	1899	8.8	171.6	25
159	US-10-101-464A-159	σ	1457		173	24
Sequence 7, Appli	JS-10-101-464A-7	σ	2432		174.6	23
Sequence 9, Appli	US-10-101-464A-9	σ	3239	9.5	178.4	22
Sequence 808, App	US-09-938-842A-808	σ	1878	6.3	180.2	21
Sequence 4, Appli	US-10-101-464A-4	σ	2868	9.4	182	20

## ALIGNMENTS

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Squence 1, Application US/1008£464

Publication No. US2020199218A1

GENERAL INFORMATION:

APPLICANT: GORING, Daphne R. et al.

ITLE OF INVENTION: PROLINE RICH EXTENSIN-LIKE RECEPTOR KINASES

FILE REFERENCE: P. 55,762-A USA

CURRENT APPLICATION NUMBER: US 10/069,364

PRIOR APPLICATION NUMBER: US 10/069,364

PRIOR PILING DATE: 2000-02-19

PRIOR PLILOGATION NUMBER: US 60/149,465

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR PLILOGATION NUMBER: US 60/159,122

PRIOR PLILOGATE: 1999-08-19

PRIOR PLILOGATE: 1999-08-19

PRIOR PLILOGATE: 1999-08-10-13

NUMBER OF SEQ ID NOS: 27

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Pred. No. 0;
                                                                                               Mismatches
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                                                                                     Best Local Similarity 100, Matches 1944; Conservative
            napus
                           NAME/KEY: CDS

LOCATION: (1)..(2189)

OTHER INFORMATION:

US-10-086-464-3
TYPE: DNA
ORGANISM: Brassica
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CCAGABATATGCTTCAAGCGGTAAATTAACCGAGAAATCCGATGTTTTCTCTTACGGAGTT 1416
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TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

FILE REFERENCE: P 25,762-A USA

CURRENT APPLICATION NUMBER: US 10/086,464

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: DCT/CA00/00966

PRIOR PILLING DATE: 2000-02-19

PRIOR FILLING DATE: 2000-02-19

PRIOR PILLING DATE: 2000-08-19

PRIOR PILLING DATE: 1999-08-19

PRIOR PILLING DATE: 1999-10-13

PRIOR PELLING DATE: 1999-10-13

SOFTWARE: PREMIN NUMBER: US 60/159,122

SOFTWARE: PREMIN VOR: 2.1

SOFTWARE: PREMIN VOR: 2.1
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; Publication No. US20020199218A1
; GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-10-086-464-9
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Matches 747; Conservative
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US-10-086-464-9
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                                                                APPLICANT SORING, Dapine R. et al.

TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REFERENCE: P. 55,762-A USA
CURRENT APPLICATION NUMBER: USA10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR FILING DATE: 2002-02-19
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1099-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-10-13
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); Mismatches 363;
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               Sequence 10, Application US/10086464 Publication No. US20020199218A1 GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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ilarity 67.1%;
Conservative
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US-10-086-464-10
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Best Local Similarity
Matches 747; Conserv
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US-10-085-464-10
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; Publication No. US20020199218A1
; GENERAL INFORMATION:
} APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR PILING DATE: 2000-09-18
; PRIOR PILING DATE: 1999-08-19
; PRIOR PILING DATE: 1999-08-19
; PRIOR PILING DATE: 1999-10-13
; NUMBER OF SEQ ID NUMBER: US 60/159,122
; NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 427.2; DB 9;
Pred. No. 1.3e-113;
0; Mismatches 413;
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Best Local Similarity 61.8%;
Matches 790; Conservative
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US-10-086-464-13
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
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Sequence 13, Application US/10086464 RESULT 5 US-10-086-464-13

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Local Similarity 51.8%;
ses 790; Conservative
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        GGGAACCTTTGGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTC
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TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REFERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/A 0.086,464
CURRENT PILING DATE: 2002-02-28
PRIOR PLILING DATE: 2002-02-19
PRIOR PLILING DATE: 2002-02-19
PRIOR PLILING DATE: 2000-08-18
PRIOR PLILING DATE: 2000-08-18
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PRIOR FILING DATE: 1999-08-19
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Pred. No. 1,3e-113;
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CTAAGATTGCTTCTGATACAAA------CACGCATGTATCAACACGTGTGGGAA
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APPLICANT: GORING, Daphne R. et al.

TITLE OF INVENTION: PROLINE-RICH EXTERSIN-LIKE RECEPTOR KINASES:

FILE REFERENCE: P 25,762-A USA

CURRENT APPLICATION NUMBER: US 10,068,454

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: PCT/CA00/00966

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 1090-108-19

PRIOR FILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 15

SEQ ID NO 15
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Pred. No. 1.3e-109;
0; Mismatches 289;
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Best Local Similarity 67.0%;
Matches 606; Conservative
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US-10-086-464-15
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TITLE OF INVENTION: PROLINE-RICE EXTENSIN-LIKE RECEPTOR KINASES
FILE REFERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR FILING DATE: 2002-02-19
PRIOR FILING DATE: 2000-02-19
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 60/159,122
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-16
SEQ PRIOR FILING DATE: 1999-08-16
SEQ ID NOS: 27
LENGTH: 2196
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Pred. No. 1.2e-109;
0; Mismatches 289;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/10086464 Publication No. US20020199218A1 GENERAL INFORMATION:
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CRGANISM: Arabidopsis thaliana
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al Similarity 67.0%;
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US-10-086-464-16
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ORGANISM: Arabidopsis thaliana
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 59.1%
Matches 644; Conservative
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LOCATION: (1)
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                                              TAGGACAAGGCGGGTTCGGTTACGTGCACAAGGTGTTGCCTAGTGGGGAAAGAAGTTG
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US-10-086-464-7
Sequence 7, Application US/10086464
Fublication No. US20020199218A1
GENERAL INFORMATION:
APPLICANT: GORING, Daphne R. et al.
TITLE OF INVENTION: PROLINE-RICH EXIENSIN-LIKE RECEPTOR KINASES
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Pred. No. 3.6e-78;
0; Mismatches 344;
FILE REFERENCE: P 25,762-B USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR APPLICATION NUMBER: PCT/CA00/00966
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR PLING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 60/149,466
PRIOR PLING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 60/159,122
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1272 TICTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCTCC 1331
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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                                                                                       DESCRIPTION OF A PROPRIED TO STATE OF A PRICE OF A PROPRIED OF A PELICANT GORING, Daphne R. et al.

TITLE OF INVENTION: PROFINE NEW BACK. NEW SET A USA CURRENT FILING DATE: 20.2-28

FILE REFERENCE: P 25.752-A USA CURRENT FILING DATE: 20.2-02-19

PRIOR PILING DATE: 20.2-02-19

PRIOR FILING DATE: 20.0-08-18

PRIOR FILING DATE: 19.99-08-19

PRIOR FILING DATE: 19.99-08-19

PRIOR FILING DATE: 19.99-10-13

PRIOR FILING DATE: 19.99-10-13
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Pred. No. 3.7e-78;
0; Mismatches 344;
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US-10-086-464-6
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Best Local Similarity 59.1%;
Matches 644; Conservative (
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2106 ATTGTACAGT 2115
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 6
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Sequence 366, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Harper, Jeff

APPLICANT: Harper, Jeff

APPLICANT: APPLICANT: SAME, NUD

APPLICANT: APPLICANT: SAME, NUD

TITLE DE INVENTION: SAME, AND METHODS OF USE

TITLE PERFERENCE: 2001-08-24

CURRENT FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER: OF SEQ ID NOS: 5379

SEQ ID NO 366

LENGTH: 1950
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ORGANISM: Arabidopsis thaliana
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Best Local S
Matches 370,
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TITLE OF INVENTION: STRESS-RECOLLATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR PILING DATE: 2000-08-24 PRIOR FILING DATE: 2000-08-24 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NOS: 5379
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Pred. No. 7.4e-49;
0; Mismatches 289;
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                                                                                                                                                                                                                                                                                                                                              tch 10.5%;
al Similarity 57.2%;
394; Conservative
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Best Local Similarity
Matches 394; Conservat
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RESULT 12 US-09-938-842A-366

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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Budworth, P.
APPLICANT: Budworth, P.
APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: Chang, X.
TATLICAN: Rang, X.
TITLE OF INVENTION: Promoters for regulation of plant expression FILE REFERENCE: 1360.001018.
CURRENT FILING DATE: 2001-06-25
FRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
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Pred. No. 6.6e-46;
0; Mismatches 312.
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                           Sequence 179, Application US/09887576 Patent No. US20020144047A1
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US-09-887-576-179
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Best Local Similarity 55.5%;
Matches 401; Conservative (
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US-09-887-576-179/c
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LENGIH: 2004
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                                                                                                GENERAL INCORMATION:
APPLICANT: BATPET, Jeff
APPLICANT: RATEPS, JOE1
APPLICANT: Areps, JOE1
APPLICANT: Anny, Xun
APPLICANT: Anny, Xun
APPLICANT: Anny, Xun
APPLICANT: Anny, Xun
APPLICANT: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
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                                                               US/09938842h
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Best Local Similarity 56.9%;
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SEQ ID NO 1911
                                                               Sequence 1911, Application Patent No. US20020160378A1
                                        US-09-938-842A-1911
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1080 CCATGG-----CGAGGGACGGCCTACAATGGAAGGAGCACCAGATTGAAGATTGCTCT
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Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: HIGORATION:

APPLICANT: Marge, Juel

APPLICANT: Wange, Xun

APPLICANT: APPLICANTON: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS

CURRENT APPLICANTON: SORE, AND METHODS OF USE

FILE OF INVENTION: SORE, 2001-08-24

CURRENT APPLICANTON NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1079
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           GCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCT
                                                                                 CCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTT
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KEYWORDS
                                                                                                 ORGANISM
                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
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ORIGIN
                                                                                                                                                                AUTHORS
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3G596561
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                                                                  /note="Vector: pBluescript SK(-); Site_1: BCORI; Site_2: Mol; supplier: Corneal University, Tankaley lab: Sequencing: The Institute for Genomic Research. Boots were isolated from in vitro grown stem cuttings on CM medium. Cuttings from in view grown stem cuttings on CM medium. Cuttings from in view grown plants on medium. It is the stem cuttings from in view grown plants on medium."
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                                                                                                                                                                                     Score 442.2; DB 13; Length 759;
Pred. No. 1.6e-95;
0; Mismatches 198; Indels 0;
     /clone="cpR033021"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGTATCACTGICAGATCTTAACGAAGGGATGAGACCAGG 1691
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ilarity 73.9%;
Conservative (
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Best Local
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RESULT 2

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Soldium tuberosum

Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Epermatophyta: Magnoliophyta; endicoryledons; core endicots;
Asteridae: euasterids I; Soldiales; Soldiaceae: Soldium.

E 1 (bases 1 to 757)
S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
Al Dipublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1800711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pBluescript SK(-); Site_1: BcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
        EST 12-APR-2001
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757 bp mRNA linear EST 12-APR-200 CSTS Solanum tuberosum CDNA clone CSTS15A23 5' sequence,
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/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.1%; Score 429.6; DB 12; Length 73.4%; Pred. No. 1.7e-92; Ive 0; Mismatches 199; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS15A23"
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1. .757
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                                                     mRNA sequence.
BG596561
BG596561.1 GI:13614701
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Best Local Similarity 73.4
Matches 549; Conservative
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IACTIGGCICCGGAAIACGCIGCAAGCGGAAAGCICACGGAGAAGICIGACGIITICICA 1380
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; endicotyledons; core endicots; assidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 692)

Wing, R.A., Frisch.D., Yu,Y., Main,D., Rambo,T., Simzons,J., Henry, D., Wood,T.C., Leslie,A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                    TATTIGGCTCCAGAATATGCTTCCTCTGGAAAGCTTACAGACAAGTCAGACGTATTCTCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:29729"
/clone='6A_Ea0012C15f'
/clone_11b='6Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                           TTTGGGGTTGTGCTTTTGGAGCTCATTACTGGACGCCGGTGATGCCAACAATGTC
                                                                                                                                         481 TTTGGIGTAATGCTTCTTGAGTTGATAACTGGACGTCGGCCTGTTGACTCTACTCAATCA
                                                                                                                         1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA
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/organism="Gossypium arboreum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tal: 864 656 4293
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Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                  ATGACACGTTCTCCGAGCCTTGGAAG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seg primer: PAATACGACTACACACATAGGG
High quality sequence stop: 690.
Location/Qualifiers
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138 c 17
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75.4%;
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Matches 514; Conservative
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CITCCTCCACCGTCTCCAGGGCTTGTGTTTAGGCTTCTCCAAAAGCACTITCACATACGAG 798

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584 pp mRNA linear EST 07-SEP-2000 AV543493 Arabidopsis thaliana roots Columbia Arabidopsis thaliana coots AV543493 Arabidopsis thaliana AV543493 AV543493
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Kazusa DNA Research Institute
Yana 1532-3, Klsazaru, Chiba 192-0812, Japan
Bmail: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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CITCCGCCTGCGTCACCTGGTATTTCCTTAGGTTTCTCGAAAAGCACTTTTAGCTATGAA
                                                                                                                                        GAATTAGCGAGGGAACGGATGGCTTCTCGGAAGTTAACCTTCTTGGACAAGGTGGTTTT
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                                                                                                                                                                                                                                                 1523 ATGCAAAGATGAATAATGGGTATGACAGAGGAGATGGCTCGCATGGTTGCTTGTGCTG 1582
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                                                         /clone="R2201f07F"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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                      /organism="Arabidopsis
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                                  /strain="Columbia"
/db_xref="taxon:3702"
Location/Qualifiers
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                                                                                                                                                                                                                                                                             /strain="AKA"
/cultivar="8400"
/db_ars="faxon:29129"
/clone="fa=1012016r"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
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/note="Yector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
134 c 167 g 187 t
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Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 646
Seq primer: TANTACGACTCACTATAGGG
High quality sequence stop: 666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.6%; Score 400; DB 13;
ilarity 75.6%; Pred. No. 2.1e-85;
Conservative 0; Mismatches 160;
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HTC 25-MAY-2002
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Peprantophyta; Aganoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1053)
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Oppublished (2002)

2 (bases 1 to 1053)
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 376; DB 11; Length 1053; 68.5%; Pred. No. 1.5e-79;
                                                                                                                                                                                                                                                                                                               linear
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/db_xref="MaizeDB:637889"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                             1053 bp. sequence.
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Zea mays PCO134818 mRNA
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                                                                                                                                                                                                                                                                                                        Chases I to 573 
                                                                     EST 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yana 1532-3, Xisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                               873 bp mRNA linear EST 06-SEP-200 aV551753 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNA clore RZ13Cc07R 5', mRNA sequence.
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/tissue_type="roots"
/note="Yector: pBluescriptII SK-; Site_1: EcoR; Site_2:
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Pred. No. 3.5e-85;
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="RZ130c07R"
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CTICTGGCAAGCIAACAGAAAAICCGAIGTATTTTCCTTCGGAGTCATGCTTCTTGAGC 310
                                                                                               25-MAY-2002
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                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Paccelad; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1016)
Hainey,C.F., Dolan,M., Miao,G.B., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                          ACTIGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTTGAGGTTTAGCTG
                                                                                                                                    ATGCAAAGATGAATAATGGGTATGACAGAGAGAGATGGCTCGCATGGTTGCTTGTGCTG
                           TCATTACTGGACGTCGACCCGTTGATGCCAACAATGTCTATGTAGATGACAGCTTAGTTG
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Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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/organism="Zea mays"
/db_xref="MalzebB:637888"
/db_xref="taxon:4577"
/clone="PCO134814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Los mays PCO134814 mRNA sequence. AVI08243 AVI08243.1 GI:21211321 HTC.
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Unpublished (2002)
2 (bases 1 to 1016)
Coe,E.C.
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assembled by DuPont as part of a collaboration for the Overgo addressing of BACs in conjunction with the Maize Mapping Project" 231 c 262 g 262 t
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                                                                                                                          DB 11; Length 1016;
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Pred. No. 3.3e-77;
0; Mismatches 238;
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(bases 1 to 652)
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Best Local Similarity 71.8:
Matches 466; Conservative
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E 1 (bases 1 to 645)

S Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Jun 10, 2002 this sequence version replaced gi:21365738.

Other ESTS: EST64428

Contact: Robin Buell

The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript SK(-); Site_1: BcoRI; Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes tibers, or 104 c 154 g 192 t
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                                                                                                                                                                                                                                                                 9712 Medical Center Dr. Rockville, MD 20850, USA
Email: points districtions
This close is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of potato cDNA clones for
tissues"
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/clone_lib="Generation of a set of
microarray analyses mixed potato ti
/tissue_type="mixed tissues"
/lab_bost="Solna"
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/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
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ilarity 74.3%;
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
J.P., Kolkman, J., Slabaudh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenonics.ucdavis.edu/
Intp://compgenonics.ucdavis.edu/
Onpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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Tel: 1-(530)-742-1742
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Bmail: akozik@atgc.org [michelmore@vegmail.ucdavis.edu/
belongs to contig OG_CA_Contig2262, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                          GGBI0120.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone QGBI0120, mRNA sequence.
BQ849683.
BQ849683.1 GI:22235152
EST.
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1381 TITGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCGTTGATGCCAACAATGTC 1440
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                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids II, Asterales, Asteraceae, Lactuceae,
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/clone="QCB10120"
/clone="QCB10120"
/clone_lib="QC_ABCDI lettuce salinas"
/lab host="E.coli"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                    Gaps
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0; Mismatches 183;
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TAG_TISSUE=roots
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Plate: QGBL0 row: I column: 20.
Location/Qualifiers
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127 c 157 q
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us-10-086-464-1.rst

High quality sequence stop: 541 POLYA=No. Iocation/Qualifiers	/db_xref="taxon:4558" /clone_lib="Embryo   (EM1)" /note="Organ: Embryos germinated for 24 hr; Vector: pBluescript II from Lambda Zap II; Site_l: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were	-	Query Match Best Local Simi Matches 432;	771 CITCICCAAAAGCACITTCACAIACGAGGAGCIAGCIAGAGCCACCAAIGGITTCICCGA	831 GGGRACTTGTTAGGRCAAGGCGGGTTCGGTTACGTCCCAAAGGTGTGTTGCTTAGTGGTTGTTCGTTGCTTGTTGTTTGGTTTTTGGGTATGTTCACAGAGGTTGCTTCATAGTTTGCTTCACAGAGATTGCTTCATAATGTTCACAGAGATTGCTTCATAATGTTCATAATGTTCATAATGTTAATGTTCAAAGGTAATGTTAATGTTCAAAGGTAATGTTAATGTTCAAAGGTAATGTTA	891 GAAAGAAGTTGCTGTAAAGTTTGAGAGTGGTCAGGAAGAGGGAGTTTCA 	OY 951 GGCAGAGGTTGAGAGCTGCAGCAGGCATCTGGTGTTGTTGGTTA 1010  10	QY 1011 IIGCALCGCGGIGCCAAAAGAIIGCITGTCTATGAGTIIGTICCTAACAACAACTGCA 1070	Qy 1071 GCTTCACCTCCATGGCGACGCCCTACAATGGAATGGACCACATTGAAGATTGC 1130  Db 317 GTTCCACTTGCAAAGATCGACCAACAATGGAGTGGCCCACTAGATTAAAGATCGC 376	OY 1131 TCTTGGATCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATCA 1190	QY 1191 CCGTGADATCAAGGCTTCAAACATATTGATAGATTTCAAGTTTTCAAGGTTGCTGA 1250   1111	OY 1251 TITGGTCTTGCTAGTTGCTTCTGATACAACAGCATGTATCAACAGGTGTGTGG 1310	QY         1311 AACCTTTGGGTACTTGGCTCCGGAATACGC 1340           DD         557 CACCTTTGGGTATTTGCGCCTGAGTATGC 586	BQ240617	Takos Triticum aestivum cDNA H::20436493	
PST GAGAGGGAGTTTCAGGCAGAGGTTGAGATCATCAGCAGAGTTCACCACAGGCATCTGGTG 996  DATE	DD	OY 1117 AGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAAT 1176	CY 1177 CCTAAAATCATTCACCGGATATCAAGGCTTCAAACATATTGATAGATTTCAAGTTTGAA 1236 [	OY 1237 GCTAAGGTTGCTGATTTTGGTCTTGCTAAGATTGCTTCTGATACAAAACACGCATGTATCA 1296 	QY 1297 ACACGTGTGGAACTTTGGGTACTTGGCTCCGGAATACGCTGCAAGGGAAAGCTC 1356	OY 1357 ACGGACAAGTCTGACTTTCTCATTTGCGTTGTGCTTTTGGAGCTCATTACTGGACGT 1416	OY 1417 CGACCCGITGAIGCCAACAAIGICTAIGIAGAIGACAGCITAGIIGACTGGGCACCACA 1476	OY 1477 TIGCITAACCGAGCATCTGAGGAGCTTTGAGGGTTTAGCTGAAGATGAAT 1536	OY 1537 AATGGTATGACAGAGAGACGCICGCATGCTTGCTTGTGCTGCGG 1585	RESULT 11 BF176907	LOCUS BF176907 593 bp mRNA linear EST 31-OCT-2000 DEFINITION EML_4_B10.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA sequence sequence.	Σ		AUTHORS Reid, S.P., Cordonnier-Pratt, MH., Gingle, A. and Pratt, L.H. TILE An EST database from Sorghum: developing embryos JOHRNAL Unpublished (2000) COMMENT Contact: Cordonnier-Pratt MM	Taboratory for Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 543 10710	Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV

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BQ134241 637 bp mRNA linear EST 19-APR-2002 1091014D01.72 1091 - Immature ear with common ESTs screened by Schmidt lab Zea mays CDNA, mRNA sequence.
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1 (bases 1 to 637)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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/corganism="rea mays"
/cultivar="0H43" was mays"
/db_xref="taxon:4577"
/clone_lib="1091 - Immature ear with common ESTs screened
y schmidt lab"
/tissue_type="Inflorescence meristem - floral organ
primordia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Immature ear; Vector: pAD-GAL4; Site_1:
EcoR1; Site_2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."
             552 GGATGGTAACTATGATGAGTTAGTGGATGCTCGTCTGG3AAAGGATTTCAATCTAATGA 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 GGCICCGACIACICGGACCGICCAGIICTICCICCACCGICTCCAGGGCIIGIGIIAGGC 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%; Score 348.2; DB 14; Length 637; 73.2%; Pred. No. 5.9e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091014 row: D column: 01.
                                                   1557 GATGGCTCGCATGGTTGCTTGTGCTTGTG 1591
                                                                        612 GATTGCCAGAATGATAGCATGTGCTGCTGCAGGTG 646
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/lab_host="Stratagene XLOLR"
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EST.
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es 446; Conserv
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                                  Wheat functional genomics - Glenlea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Eax: (204) 983-4604
Email: scloutier@em.agr.ca
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                                                                                                                                                                                    was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >2.0 kb Plate: 015 row: B column: 02 Seq primer: MI3 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="E. coli DH108"
/note="Vector: pSPORT-P (Invitrogen Technologies);
NotI; Site_2: Mulu: mRNA obtained from wheat seeds cultivar Glenlea 5 days post-anthesis"
126 c 162 g 189 t
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Pred. No. 4.8e-73;
0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                  /organism="Triticum aestivum"
/cultivar="Glenlea"
/db_xref="taxon:4565"
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Best Local Similarity 71.8%;
Matches 456; Conservative
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DOSSIGO4.NG.abl 0G_EFCHJ lettuce serriola Lactuca sativa CDNA clone 0GG21G04, maka sequence.
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Lettuce and Sunflower ESTs from the Compositae Genome Project Unpublished (2002)
                                     629 CACTACCACCACCTAAGGCTCCATCTCCACGGCAACCTCCTCCACCACCACCAC 688
                                                                                                                                               61 TCATTAGCAGAGATGGGAGGTTCTGGCTCTAATTATTCAGGTTCTGAAAACCCGCTTCCGC 120
                                                                                                                                                                                                                        121 CICCGICACCIGGIATITCCITAGGITICICGAAAGCACTITIAGCIAIGAAGAATTAG 180
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids II, Asterales, Asteraceae, Lactuceae,
                                                            CACCGICICCAGGGCITGIGITAGGCITCICCAAAAGCACITTCACATACGAGGAGCIAG
                                                                                                                                                                                                                                                                                                181 CGAGAGCAACGGATGGCTTCTCGGAAGTTAACCTTCTTGGACAAGGTGGTTTTGGGTACG
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Mismatches 198;
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   Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; Osre eudicots;

Rosidae; eurosids II; Malvales; Malvacea; Gossypium.

E 1 (bases 1 to 679)

SW Wing,R.A., Firsto,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry, J., Wood,T.C., Leslie,A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and erolution of the cotton fiber

Of the cotton fiber

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                 CTIGGATCIGCTAAAGGACTITCTIATCTICATGAAGATIGCAATCCTAAAAICATTCAC 1191
                                                                                        1251
                                                                                                                                                                                                                                                                                                                    TTTGGTCTTGCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGA 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 22-MAY-2002
                 TGCATCGCCGGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGGAG 1071
                                                                                                                                                                                                                                                                               568
                                                                                                                             448
                                                                                                                                                                                                                                                                                                                                          BQ404121 679 bp mRNA linear EST 22-MAY-2003 GA_Ed0066E04f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ed0066E04f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="GA_Ed0066E04f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                     CGTGACATAAAGGCATCTAACATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGAT
                                                                                                            389 TTCCACTTACATGCGAAAGTCGACCAACAATGGAGTGGCCTGCTAGATTAAAGATCAGT
                                                                                                                                                                                                    449 TTGGGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCAT
                                                                                                                                                                                                                                       1192 CGTGATATCAAGCCTTCAAACATATGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
Fotal High Quality bases = 516
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TAATACGACTCACTAIAGGG
High quality sequence start: 4
High quality sequence stop: 646.
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Pred.
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/cultivar="8400"
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EST.
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70.4%;
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Tel: 864 656 7288
Fax: 864 656 4293
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Gaps 'n 805

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/note="Vector: pBECDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5° and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=QG_ERGHJ lettuce serriola TAG_LIB=QG_ERGHJ lettuce serriola TAG_LIB=QG_ERGHJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 CCGGCCCTATTTAACAGCGGTGCTTCCGGTTCCAACTATTCCGGCGGTTCAAACCCTCTT 193
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Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Erax: 1-(530)-752-9659
Erax: 1-(530)-752-9659
Erax: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig2262, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    862 TACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTTGCTGTGAAGCAGTTGAAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="2GG21G04"
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Location/Qualifiers
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        QY
        1162 CATGAAGATTGCAALCCTAAAATCATTCACCGTGATATCAAGGCTTCAACATATTGATB 1221

        Db
        614 CATGANGATTGCAACCTACTCTCGAGATATAAAAGCTGCTAATATACTTCTT 673

        QY
        1222 GATTCAAGTTGCAAGATCATTTGGTCTTGCTAAGATTGCTTCTGTAACATTCTT 673

        Db
        674 GATTCAAGTTTGAAGCTAACGTGCTGATTTTGGTCTTGCTAAGATTCCCCGAT-GT 732

        QY
        1282 AACACGCATGTAACAAGGTAGCGGAACTTTGGGCTTGCGAAGATACTCCCCAT-GT 732

        QY
        1282 AACACGCATGTAACAAGGTAGCGAACTTTGGTTTTGGTTGCTAAGATTTCCCCAT-GT 732

        Db
        733 GCCACTCATGTCCACCCGTGTGATGGGAAGTTTTGG 7319

        Db
        733 GCCACTCATGTCCCCACGTGTGATGGGAAGTTTTGG 770
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Search completed: July 7, 2003, 10:26:51 Job time : 2874 secs

Tue Jul

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 15:16:17; Search time 25 Seconds (Without alignments) 1073.407 Million cell updates/sec July Run on:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST.....REMEMGKIKRTGQGYSGPSL 647 Title: Perfect score:

Scoring table: Sequence:

112892 segs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length; 0 Maximum DB seq length; 200000000

Post-processing: Minimum Match 0%
Maximum Match 186%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	006548 arabidopsis	arabidopsi	3 arabidopsi	m	'n	arat	a	P47735 arabidopsis		P17801 zea mays (m		chlam			P13983 nicotiana t	P05143 mus musculu	_4	h epi		homod		Q03211 nicotiana t			Q9m1g9 arabidopsis		Q04982 gallus gall		P24152 sorghum bic	042632 cochliobolu	O43187 homo sapien		043516 homo sapien
SUMMARIES	a	APKA ARATH	APKB_ARATH	TMK1_ARATH	NAK_ARATH	CRI4_MAIZE	CLV1_ARATH	SRK6_BRAOL	RLK5_ARATH	IRA1_MOUSE	KPRO_MAIZE	IRA1_HUMAN	GP1_CHLRE	TML1_ARATH	KPEL_DROME	EXTN_TOBAC	PRP3_MOUSE	CRK7_HUMAN	DDR1_HUMAN	EXTN_MAIZE	MUC2_HUMAN	PRP2_MOUSE	EXLP_TOBAC	RMIL_COTJA	KYK1_DICDI	EXT2_ARATH	DDR1_MOUSE	RMIL_CHICK	DDR1_RAT	EXTN_SORBI	KPC1_COCHE	IRA2_HUMAN		WAIP HUMAN
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Q05609 arabidopsis	P04280 nomo sapien P07527 schizosacch	Q9jlO4 mus musculu	O60610 homo sapien	P06599 daucus caro	P46551 caenorhabdī	P28693 gallus gall	008808 mus musculu	P48562 saccharomyc	P23246 homo sapien	P37370 saccharomyc
CIRI_ARATH	WEEL_SCHPO	FMN2_MOUSE	DIA1_HUMAN	EXTN_DAUCA	CDK9_CAEEL	SPB2_CHICK	DIA1_MOUSE	CLA4_YEAST	SFPO_HUMAN	VRP1_YEAST
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315	311	310.5	307	306.5	300.5	300.5	297.5	297	296.5	296.5
34	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 APKA_ARATH APKA_ARATH STANDARD; PRT; 410 AA.		Protein kinase ARKIA (EC 2. APKIA.	Arabidopsis thaliana (Mouse-ear cress).		OC eurosids II; Brassicales; Brassicaceae; Arabidopsis. OX NCBI TaxID=3702;		STRAIN=cv. Columbi	MEDLINE=93081726;	RA Hirayama T., Oka A.; RT "Novel protein kinase of Arabidopsis thallana (APK1) that	phosphorylates tyrosine, serine and threonine.";	Plant Mol. Biol. 20:653-662(1992).	SERINE/THREONINE ACTIVITY. IN VIVO, CAN PHOSPHORYLATE	CC RESIDUES OF LIMITED SUBSTRAINES.		ISS-PROT entry is copyright. It is produced through a c	the Euro	use by non-profit institutions as long as its content is in no	modified and this statement is not removed. Usage by	encicles requires a incense or send an email to license		DR EMBL; D12522; BAR02092.1; DB Infordate: Indefendit Brit Afface			Pfam, PF00069; pkinas		PROSITE; PS00107;	PROSITE; PS00108; PROTEIN_KINASE_ST; 1	DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. XW Transferase; Serine/threonine-protein kinase: Tyrosine-protein kinase:	ATP-binding, Multigene family, Myristate.	FT LIPID 2 2 MYRISTATE (BY SIMILARITY).	NP RING 74 82 APP (BY	BINDING 106 ATP (BY	FT ACT_SITE 203 203 BY SIMILARITY. SO SECURING 410 AA: 45519 WW: SPARSENGESORSORS.	ישה כדרכז ישי סדי קסויים איני
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Score 556.5; DB 1; Length 410; Pred. No. 1.4e-18;

19.0%; 39.1%;

Query Match Best Local Similarity

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63 FKGWIDEKSLIASRPGTGLVIAVKKLNQDGWQGHQEWLAEVNYLGQFSHRHLVKLIGYCL 142
                                                                                                                                                                                                                                                                                      260
                                    ---SPGLVLGFSKSTFTYEELARAINGFSEANLLGQGGFGYV 289
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                                                                                                                                                                                            SDYYSEGVVLLELLSGRRAVDKNRPSGERNLYEWAKPYL--vnkrkifr-vidnklqdqy
                                                                                                                                                                                                                                                                                                                                                                                 516 DREEMARMYACAAACVRHSARRPPRMSQIVRALEGNVSLSJLNEGMRPGQSNVYSSYGGS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CY. Columbia;
MEDLINE-2008487; PubMed=10617197;
MEDLINE-20084887; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldilyum T.V., Budli C.Y., Katchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Budli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Tallon L.J., Gill J.S., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
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TYROSINE
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SERINE/THERONINE ACTIVITY. IN VIVO, CAN PROSPHORYLATE TYROSIN
RESIDORS OF LIMITED SUBSTRATES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence and analysis of chromosome 2 of the plant Arabidopsis
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 131; Indels
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-!- FUNCTION: POSSIBLE BI-FUNCTIONAL KINASE. IN VITRO, IT
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-3001 (Rel. 40, Last annotation update)
APCHE OR AT2G28930 OR T914.1.
   63; Mismatches
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MEDLINE=93081726; PubMed=1450380;
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   Conservative
                                  GSDYSDRPVLPPP--
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P46573; Q9SLH5;
01-NOV-1995 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
      a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 PPPPPPFMSS----SGGSDYSDRPVLPPP-----SPGLVLGFSKSTFTYEELARAIN 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; Multigene family; Myristate.

LIPID 2 2 MYRISTATE (BY SIMILARITY).

DOMAIN 69 356 PROTEIN KINASE.

MP_BIND 75 83 AIP (BY SIMILARITY).

BINDING 107 107 ATP (BY SIMILARITY).

ATP (BY SIMILARITY).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative receptor protein kinase TMK1 precursor (EC 2.7.1.-).
TMK1 OR AT1356150 OR F15E12.4.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 412;
 SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    EB1CA0B1A626A5DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.0%; Score 654.5; DB 1;
41.3%; Pred. No. 1.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 113;
                                                                                                                                 EMBL: D10152; BAA20968.1.; ...
InterPro: IPR004040; STV_pkinase.
InterPro: IPR004040; STV_pkinase.
InterPro: IPR001299; Ser_thr_pkinase.
InterPro: IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; BUK_pkinase; 1.
SWART; SM0021; STYRC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
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RECEINE-21016719; PubMed=11130712;

RELINE-21016719; PubMed=11130712;

RELINE-21016719; PubMed=11130712;

RELINE-21016719; PubMed=11130712;

RA Theologias A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Thite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Thite O., Alonso J., Conway A.R., Creasy T.H., Dewar K.,

ROBING M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

ROBING M.K., Conn L., Conway A.B., Hughes B., Huizar L.,

RA Thiter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Link S.J. Liu S.X., Luros G.S., Malti R., Mazziali A.,

RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Radano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Ru J. Tun Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

Ru J., Wallen D., W., Venter J.C., Davis R.W.;

Rubliana., S., Vaysberg M., Vysotskaia V.S., Walker M.,

Rubliana., S., Vaysberg M., Vorus M., Rabidopsis
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Eukaryota, Viridiplantae, Streptophyta; Emoryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                           STRAIN-cv. Columbia;
WEDITRE=930510; Publed=1332795;
Chang C., Schaller G.B., Patterson S.E., Kwok S.F.,
Keyerowitz E.M., Bleecker A.B.;
"The TMK1 gene from Arabidopsis codes for a protein with structural and biochemical characteristics of a receptor protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: PROBABLE RECEPTOR.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: FOUND IN MOST TISSUES.
-!- PTM: AUTOPHOSPHOSPHATED ON SERINE AND THREOMINE RESIDUES.
-!- PTM: AUTOPHOSPHOSPHATED OF SERINE AND THREOMINE RESIDUES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: CONTAINS 9 LEUCINE-RICH REPERATS (LRR).
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Transmembrane; Receptor; Glycoprotein; Signal; Repeat;
Leucine-rich repeat; Phosphorylation.
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DCM; 1.
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InterPro: IPR004040; STY_pkinase.
InterPro: IPR00290; Ser_thr_pkinase.
Pfam: PF00569; Pkinase; 1.
Pfam: PF00569; LRR: 11.
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SWART; SM00370; LRR; 7.
SWART; SW00369; LRR_IYP; 1.
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InterPro; IPR000719; Euk pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC026480; AAG51302.1; -.
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InterPro; IPR003592;
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                                                                             NCBI_TaxID=3702;
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PUTATIVE RECEPTOR PROTEIN KINASE TMK1
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                      EXTRACELLULAR (POTENTIAL).
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                                                       CYTOPLASMIC (POTENTIAL)
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RY Tablare. L. Karekor T., Nakamura Y., Kotani H., Kato T., Asamizu E.,

RA Tabata S., Karekor T., Nakamura Y., Kotani H., Kato T., Asamizu E.,

RA Mayajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,

RA Mayazaki N., Naruoto M., Matsuno A., Muraki A., Nakayama S.,

RA Makazaki N., Naruoto M., Matsuno A., Muraki A., Nakayama S.,

RA Matabe A., Yamada M., Yasuda M., Sato S., Takeuchi C., Wada T.,

RA Huang E., Spiegel L., Golo, L., O'Shauqinessy A., Preston R.,

RA Hang E., Spiegel L., Golo, L., O'Shauqinessy A., Preston R.,

RA Hang E., Cordum H., Cordes M., Courtney W., Dante M.,

RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,

Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,

RA Belter E., Cordum H., Cordes M., Hoon See L., Vil D., Baker J.,

RA Namer-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,

RA Martienssen R., McCombie W.R., Milson R.K., Murphy G., Bancroft I.,

RA Martienssen R., McCombie W.R., Milson R.K., Murphy G., Bancroft I.,

RA Martienssen R., McCombie W.R., Milson R.K., Murphy G., Bancroft I.,

RA Gaveren M., Dirkse W., Mooijman P., Klein Lankhorst R.,

Ransperger U., Wedler H., Balke K., Weilor E., Johnson S.,

Ransperger U., Medler H., Balke K., Welein Eankhorst R.,

Ransperger U., Medler H., Balke K., Welein Eankhorst R.,

Relizenegger T., Bothe G., Rose M., Hauf J., Bernes S., Hempel S.,

Relizenegger T., Bothe G., Rose M., Mayer K.F.X., Rudd S., Schoof H.,

Ransperson M., Lamberth S., Willarroel R., Gielen J., Ardiles W.,

Ransperson M., Lamberth S., Willer R., Bevan M., Fransz P.F.;

Ry Feldpausch M., Sequence and analysis of chromosome 5 of the plant Arabidopsis
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                                                                                       P43293; Q9L296;
01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine/threonine-protein knase NAK (BC 2.7.1..).
NAK ON AT5G02930 OR TEE22_50.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Varidiphantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnollophyta; eudicotyledoms; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moran T.V., Walker J.C., "Molecular cloning of two novel protein kinase genes from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:823-826(2000).
-!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF PLANT GROWIH AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: ROOTS, LEAVES AND STEMS.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                         389 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1216:9-14(1993).
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EMBL; AL162874; CAB85534.1; ...
Interpro; IPR000719; EUK_pkinase.
Interpro; IPR004040; STY_pkinase.
Interpro; IPR00290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=94032493; Pubmed=8218420;
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                                                                                                                                                                                                                                                                                                                                                                                                        eurosids II; Bra
NCBI_TaxID=3702;
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                                                                  NAK ARATH
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RESULT 4
NAK_ARATH
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ProDom; PD000001; Euk\_pkinase; 1.

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                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                       23 FLSRDGSKGSSTASFSYMPRIEGEILONANIKNFSLSELKSATRNFRPDSVVGEGGFGCV
                                                                                                                                                                                                                                                                                                                                          290 HKG-----VLPS----GKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCI
                                                                                                                                                                                                                                                                                                                                                               143 EEBHRLLVYEFMTRGSLENHLFRRGTFYQPLSWNTRVRMALGAARGLAFLH-NAQPQVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 RDIKASNILIDFKFEAKVADFGLAKIA-SDINTHVSTRVMGTFGYLAPEYAASGKLIEKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                 Gaps
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MEDLINE=96355669; PubMed=8703079;
Becraft P.W., Stinard P.S., McCarty D.R.;
"CRINKLY4: A TNFR-like receptor kinase involved in maize epidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Putative receptor protein kinase CRINKLY4 precursor (BC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLUIAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS I TWFR-CYS REPEAT.
                                                                                                                                                                                                                                               19:
                                                                                                                                                                                                             Length 389;
SMART: SM00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/fureonine-protein kinase; ATP-binding. DOMAIN 68 353 PROTEIN KINASE; ATP-binding. HP_BIND 74 82 ATP (BY SIMILARITY).
                                                                                                                                         BY SIMILARITY.
G -> V (IN REF. 1).
58A11A78515898E3 CRC64;
                                                                                                                                                                                                           18.1%; Score 626.5; DB 1; 41.1%; Pred. No. 1.7e-17;
                                                                                                                                                                                                                                            64; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517 REEMARWACAAACVRHSARRRPRMSQIVRALE 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 LTRALKIAVLALDCISIDAKSRPTMNEIVKTME 351
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                                                                                                                                                                            43533 MM;
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106
203
287
389 AA;
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                                                                                                                                           ACT_SITE
CONFLICT
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or send an email to license@isb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTEGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNR 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KAGDIFAILDPVLSPPSDLEALKKIASVACKCVAMRGKDRPSMDKVTTALEHALALIM 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 787 GSPCIEQPILPIETVIGSSRMHKVSQMSSNHSCSE-NE-----LADGEDQGIG-YR 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::||::|| ||::|:||| ||::||| ||::||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
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                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat; Transmembrane; Signal, SIGNAL 1 24 POTENTIAL.
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PUTATIVE RECEPTOR PROTEIN KINASE
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52F8481AC187E061 CRC64;
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AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
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82; Mismatches 129;
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                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00052; TNRR_NGRR_1; FALSE_NEG
PROSITE; PS50050; TNRR_NGRR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                     InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001368; INFR_c6.
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Pfam; PF00069; pkinase;
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SMART; SM00208; TNFR; 1
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nes 145; Conserv
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REPURINGE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CY. Columbia;

MEDLING-219, PubMed-11130712;

MEDLING-219, PubMed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Caker J.R., Palm C.J., Edward C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Bunn P., Etqu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin S., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Milscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Dai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
""
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                                                                                                                                                                                                                                                     FUNCTION: ACTS WITH CLV3 TO CONTROL THE BALANCE BETWEEN MERISTEM CELL PROLIFERATION AND DIFFERENTIATION. MAY ACT WITH CLV3 AS A LIGAND-RECEPTOR PAIR IN A SIGNAL TRANSDUCTION PATHWAY, COCODINATING GROWTH BETWEEN ADJACENT MERISTEMATIC REGIONS. SUBGNIT: MULTIMER (POTENTIAL).

SUBGNIT: MULTIMER (POTENTIAL).

TISSUE SPECIFICITY: IN A CENTRAL REGION OF THE SHOOT AND IN BARIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Landsberg erecta;
MEDLINE=97304386; PubMed=9160749;
Clark S.E., Williams R.W., Meyerowitz E.M.;
"The CLAVATAI gene encodes a putative receptor kinase that controls shoot and floral meristem size in Arabidopsis.";
Cell 89:575-585(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams R.W., Clark S.E., Meyerowitz E.M.;
Genetic and physical characterization of a region of Arabidopsis
chromosome 1 containing the CLAMATA1 gene.";
Plant Mol. Biol. 39:171-176(1999).

    -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
    -i- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).

608 NPTSDYGLYPSGSSSEGQITREMEMGKIKR 637
                                               |: ::||::||:|
|836 APS--WITFPSVTSSORRKSSASEADIVGR 863
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MEDLINE=99178804; PubMed=10080719;
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NCBL_TaxID=3702;
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(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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PRINTS; PRODOUS; ILRURCHREPT.
PRINTS; PRODOUS; ILRURCHREPT.
PRODOUS; DAN, 18.
PROSITE; PRODOUS; LAR, 18.
PROSITE; PRODOUS; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PSOULOB; PROTEIN_KINASE_DOM; 1.
PROSITE; PSOULOB; PROTEIN_KINASE_DOM; 1.
TRANSFERSES; Serine-thation; Signal; Repeat; Lewcine-rich repeat; Transferase; Serine-threonine-protein kinase; ATP-binding; Phosphorylation; Transmembrane.
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               send an email to licemse@isb-sib.ch)
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                                     EMBL; AF049870; AAD02501.1; -
EMBL, AC007356; AAR26772.1; AIT_INIT.
LILLEPPO; IPR000719; ENL_PKINASE.
InterPro; IPR001611; LRR.
                                                                   InterPro; IPR003592; LRR_out.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfan; PF00069; pkinase; 1.
Pfan; PF00560; LRR; 18.
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                             EMBL; J96879; AAB58929.1;
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Length 980;

579.5; DB 1; No. 2.2e-15;

Score :

16.88; 34.88;

Query Match Best Local Similarity

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11;
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                                                187 PYGGOOOQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPFMSSSGGSDYSDRPV 246
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SEQUENCE FROM N.A.

SEQUENCE TROWNESTIGMA:

STRAIN-CV. S6S6; TISSUB-Stigma:

MEDLINE-92020942; PubMed=1681543;

Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;

Molecular cloning of a putative receptor protein kinase gene encoded

The self-incompatibility locus of Brassica oleracea.";

The roc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).

TEUNCTION: INVOLVED IN SPORDHYTIC SELF-INCOMPATIBILITY SYSTEM

THE THABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-

FERTILIZATION), PROBABLY ACTING IN COMBINATION WITH S-LOCUS-

SPECIFIC GIYCOPROFEINS. INTERACTION WITH A LICAND IN THE

EXTRACELLULAR DOMAIN.

C. CHARLYTIC ACTIVITY: ATP + A PROTEIN KINASE ACTIVITY OF THE

C. CHARLYTIC ACTIVITY: ATP + A protein ADP + a phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 TEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPL---LNRASEQGDFEGLADA
                                                                                                --SDHNHTAL
                                                                                                                                           -GESKSTFTYEELARAINGF
                                                                                                                                                                                           636 FSPSRIVITVIAAITGLILISVAIRQMNKKKNQKSLAWKLTAFQKLDFKSEDVLEC---L
                                                                                                                                                                                                                                         276 SEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGERE--FQAEVELISRVHHRHLVS
                                                                                                                                                                                                                                                                                                                                         LVGYCLAGAKRLLVYEFVPNNNLETHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNP
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Gaps
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein.
TISSOE SPECIFICITY: PREDOMINANTI IN THE PISTIL AND ANTHER.
POLYMORPHISM: THERE ARE A NUMBER OF DIFFERRY SALLELES IN
B.CLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY.
SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
A SER/THR-PROTEIN KINASE RELATED IO RAF KINASES.
61;
65; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMNNGYDREEMARMVACAAACVRHSARRRPRMSQIVRAL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 PLGG---QFLVFNETSFAGWIYLCLPHRVSCPTRPGQT-
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139; Conservative
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BY SIMILARITY.

N'LINKED (GLCNAC. ..) (POTENTIAL.)

'T.CNAC. ..) (POTENTIAL.)
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Iransferase; Serine/threonine-protein kinase; Signal; ATP-binding;
Iransmembrane; Receptor; Glycoprotein; Self-incompatibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                   PUTATIVE SERINE/THREONINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 572; DB 1; Length 849; 32.3%; Pred. No. 3.6e-15;
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CYTOPLASMIC (POTENTIAL).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Mismatches 119;
                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                  RECEPTOR.
                                                                                                        InterPro; IPR004040; SIT_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR000858; Slocus_glycop.
                                                     EMBL; M76647; AAA33000.1; ALT_TERM.
                                                               IPR001480; B_lectin.
IPR000719; Euk_pkinase.
IPR003609; Pan_app.
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                                                                                                                                                              Pfam; PF00954; S_locus_glycop; 1.
Pfam; PF01453; Agglutinin; 1.
ProDom; P2000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97231 MM;
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SMART; SM00473; PAN_AP; 1.
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849 AA;
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RC STRINGER FROM NA.

RA SEQUENCE ROAD NA.

RA MAYER X. P.X. Schweller C., Wanbutt R., Murphy G., Volckeert G., Marcher C., Wanbutt R., Durcaterhoeft A., Stlekera W., Entindthalia T., Reper M.; Ducaterhoeft A., Stlekera W., Schweller M.; Schwiller M., Schweller M., Schwiller M., Dalsany M., Pulgdomenech P., Matson M.; Schwiller M., Ballania T., Reithert B., Portetale D., Perez-Alonso M., Boutty M., Boutty M., Bantlar T., Reithert B., Portetale D., Perez-Alonso M., Boutty M., Schwiller M., Schwiller M., Schwiller M., Schwiller M., Battlan T., Robben J., And Weller B., Ranken M., Weller B., Ranken M., Weller B., Ranken M., Weller B., And Weller B., Brandt B., Betes S., Van Staveren M., Dirkse W., Battlan D., Ranken M., Weller S., Van Staveren M., Dirkse W., Berneiser S., Hempel S., Feldpausch M., Itamberth S., Van Geter P., Berneiser S., Hempel S., Feldpausch M., Waller S., Van Staveren M., Dirkse W., Berneiser S., Hempel S., Feldpausch M., Waller S., Van Staveren M., Dirkse W., Wan Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., An Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., Ra Borkova D., Blocker H., Schare M., Grimm M., Lebhert T., E., Abelber C., Robert T., Lignori R., Pierbert M., Schwert S., Rabel C., Fends M., Mattaga W., Schaefer M., Meller T., Ender M., Schwert S., Gender M., Moller R., Schaefer M., Schwert S., Rabert C., Wonfort A., Cascuberta B., Rabert C., Wonfort M., Stock R., Rabert M., Wolffam D., Rabert S., Francs P., Berrer P., Schwert S., Scholler F., Schwert S., Scholler F., Berrer S., Francs P., Berrer S., Francs P., Berrer D., Lawran D., Hasse D., Lenfer R., Messer B., Tencon D., Torce R., Perrer Perez Perez A., Purnelle B., Berrer C., Wonfort A., Schwer S., Francs P., Berrer D., Cordes M., Authourg S., Francs P., Berrer D., Couther P., Cordes M., Barques M., Authourg S., Frank D., Schwer J., Schwer J.
                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Receptor-like protein kinase genes of Arabidopsis thaliana."; Plant J. 3:451-456(1993).
                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
15-70Nr-2002 (Rel. 41, Last annotation update)
Receptor-like protein kinase 5 precursor (EC 2.7.1.-).
RLK5 OR AT4G28490 OR F2109.180.
                                                                                                                                           999 A.A.
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
MEDLINE=94035150; PubMed=8220453;
                                                                                                                                                                                   (Rel. 33, Created)
535 ARREPRINSOIV 545
                           | || || :|
793 AEHRPAMSSVV 803
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                              01-FEB-1996
                                                                                                                                         RLK5_ARATH
P47735;
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PRT;
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Mammalia, Butheria, Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 34-710 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kopp E.B., Ghosh S.;
"Cloning of mouse IRAK.";
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
    210
269
282
452
452
576
697
711
819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                        999 AA;
                                                                                                                   Best Local Similarity
Matches 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WCBI_TaxID=10090;
    210
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711
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Q62406;
                      CARBOHYD
CARBOHYD
                                                                    ACT_SITE
MUTAGEN
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BINDING
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                                                                        "Biochemical properties of the autophosphorylation of RLK5, a receptor-like protein kinase from Arabidopsis thaliana.",
Biochim. Biophys. Acta 1208:65-74 (1994).
-!- CCFACTOR: HAVE SIGNIFICANTLY GREATER ACTIVITY IN THE PRESENCE OF MA2+ THAN MG2+.
-!- IISSUE SPECIFICITY: EXPRESSED IN ROOTS AND ROSETTES.
-!- PTM: AUTOPHOSPHORILATED ON SERINE AND THREONINE RESIDUES.
-!- PTM: AUTOPHOSPHORILATED ON SERINE AND THREONINE RESIDUES.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...) (POTENTIAL).
...) (POTENTIAL).
...) (POTENTIAL).
...) (POTENTIAL).
then E., Marra M., Martienssen R., McCombie W.R.;
Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR-LIKE PROTEIN KINASE 5. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Serine/threonine-protein kinase; ATP-binding;
Transmembrane; Glycoprotein; Phosphorylation; Leucine-rich
Repeat; Signal 14 POTEWIAL.
                                                                                                                                                          -!- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPRATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN KINASE A.F; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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N-LINKED
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N-LINKED
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EnterPro; IPR00290; Ser_thr_pkinase.
Bam; PF00069; pkinase; 1.
Pfam; PF00560; IRR; 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.0.0.0.00
                                                                                                                                                                                                                                                             EMBL; AL021749; CAA16689.1; -.
EMBL; AL161572; CAB79651.1; -.
InterPro; IPR000719; Buk_pkinase.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                       PRINTS: PRO0019; LEURICHRPT.
ProDom; PD000001; EUK_PKinase; 1.
SMART; SM00370; LRR; 17.
                                                       MEDLINE=94368830; PubMed=8086440;
Horn M.A., Walker J.C.;
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LRR
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                          Mature 402:769-777(1999)
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                                              CHARACTERIZATION.
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TRANSMEM
DOMAIN
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CARBOHYD
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258 FSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGERE-- 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------RQMEVEILSRVHHRHLVSLVGYCIAGAKRLLVTEFVPNNNLELHLHGE--GR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               726 SDSLNRDVFAAEVETLGTIRHKSIVRLWCCCSSGDCKLLVTEYMPNGSLADVLHGDRKGG 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          846 MSGSKIPEAMSGIAGSCGYIAPEIVYILRVNEKSDIYSFGVVLLELVIGKQPIDSE--LG 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 DDSLVDWARPLINRASEQGDFEGLADARMNNGYDREEMARMVACAAACVRHSARRRPRMS 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 -ASDINTHVSTRVMGTFGYLAPEYAASGKLIEKSDVFSFGVVLLELITGRRPVDANNVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIMENSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILEDFKFEAKVADFGLAKI--
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"Developmental and tissue-specific expression of mouse pelle-like protein kinase.";
"Biol. Chem. 271:17609-17612(1996).
-!- FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KINASE ASSOCIATES WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Hus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frofimova M., Sprenkle A.B., Green M., Sturgill T.W., Goebl M.G.,
                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
11c-OCT-2001 (Rel. 40, Last annotation update)
11cterleukin-1 receptor-associated kinase 1 (EC 2.7.1.-) (IRAK-1)
11RAK1 (Pelle-like protein kinase) (mPLK).
                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                11 K->E: LOSS OF CATALYTIC ACTIVITY.
109095 MW; F5793D899EA0C6A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 QIVRALE --- GNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDM 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 KVVIMEQEVSGAVPCSSPNTSKR-----SKTGGKL---SPYTTEDL 996
                                                                                                                                                                                                                                                                                                                   Length 999;
                                                                                                                                                                                                                                                                                                                                                                            61; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
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ATP (BY STMILARITY).
BY SIMILARITY).
BY SIMILARITY).
                                                           (GLCNAC.
     (GLCNAC. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPGSPPAPVTPPTRNPPPSVPGPPS-NPSREGG--SPRPPSSFSPP--SPSSDGLSTGVV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLSWPQRLDILLGTARAIQFLHQD-SPSLIHGDIKSSNVLLDBRIMPKLGDFGLARFSR 366
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                                                             DEVELOPMENTAL STAGE: EXPRESSED FROM E11 DAY TO E18 DAY.
PIM: AUTOPHOSPHORYLATED, AN EXTENSIVE PHOSPHORYLATION OF IRAK
OCCURS AFTER ITS ASSOCIATION WITH ILL1-R-1. THIS STEP COULD BE
LINKED TO THE ACTIVATION OF THE KINASE (3Y SIMILARITY).
SIMILARITY: SELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
THE II-1 RECEPTOR II1-R-1. THIS ASSOCIATION IS RAPID AND IL-I DEFENDENT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00531; death; 1.
Probom; PP00001; Buk_pkinase; 1.
SMART; SM00210; S_TKC; 1.
SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_AIP; 1.
PROSITE; PS00108; PROTEIN_KINASE_AIP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/Chreonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8A501F002CD3EBD2 CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Score 515.5; DB 1; 26.7%; Pred. No. 3.9e-13; live 75; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                           EMB., AF103876, AAD1324.1; ALT_INIT.
MGD: MGT:107420: Illrak.
InterPro: IPR0007488: Doath.
InterPro: IPR000719; Euk_pkinase.
InterPro: IPR001290: Ser_thr_pkinase.
InterPro: IPR001245; Tyr_pkinase.
Ffam: PP00069: pkinase.
Ffam: PP000631; death; 1.
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Best Local Similarity 26.7%
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                               EMBL; U56773; AAC52694.2;
                                                 AND SKELETAL MUSCLE.
                                                                                                                                                 PELLE SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              710 AA;
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SEQUENCE
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                                                           427 OGAKTKYLKDLIEDEAEEAGYTLKSTQPTLWGVATDAWAAPIAAQIYKKHLDSRPGPCP 486
       WARPLINRA-----SEQGDFE 504
                                                                                                                                                                                                    ---LAQLACC---CMHRRAKKRPPMTQVYKRLEGLQAGPPWELEV 531
                                                                                                                                                                                                                                                                                                                               532 AGHGSPSPQENSYMSTTGSAQSGDEPWQPLVVTTRAPAQAAQQIQRSPNQPVESDESVPG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                 ---GLADAKMINGYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVS----LSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walker J.C., Zhang R.; "Relationship of a putative receptor protein kinase from maize to the S-locus glycoproteins of Brassica."; Nature 345:743-746(1990).
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SIMILARIY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
A SER/THR-PROTEIN KINASE CLOSELY RELATED TO RAF KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative receptor protein Kinase ZMPK1 precursor (EC 2.7.1.37).
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-i- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE SHOOTS
ROOTS OF YOUNG MAIZE SEEDLINGS, AND TO A LESSER EXTENT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : : :| : : :| : : :| : : :| : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : : :| : : :| : : :| : : : :| : : : : :| : : : : :| : : : : :|
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Shang R., Walker J.C.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   557 INEGMRPGQSNVYSSYGGSIDYDSSQYNEDMKKFRKMALGTQE---
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Ser_thr_pkinase.
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MEDLINE=90294911; PubMed=2163028;
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Euk_pkinase.
PAN.
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   -DANNYYVDDSLVD-
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PELLE SUBFAMILY.
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712 AA;
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                                                                                                                                             PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2201 (Rel. 40, Last annotation update)
Interleuxin-1 receptor-associated kinase 1 (BC 2.7.1.-) (IRAK-1).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                        14.8%; Score 512.5; DB 1; Length 817;
                                                                                  PROSITE; PS00107; PROTEIN KINASE_AIP; 1.
PROSITE; PS00108; PROTEIN KINASE_SI; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine, Chreonine-Protein kinase; AIP-binding;
Transmembrane; Receptor; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. .) (
N-LINKED (GLCNAC. .) (
N-LINKED (GLCNAC. .) (
                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
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                                                                                                                                                                                  PROTEIN KINASE
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MEDLINE-96180673; PubMed-8599092;
InterPro; IPR000858; Slocus_glycop. Pfam; PR00024; PAN; 1. Pfam; PR00069; pkinase: 1. Ffam; PR00954; S_locus_glycop; 1. Pfam; PF01453; Agglutinin; 1. Pr0Dcm; P0000001; Buk pkinase; 1. SWART; SW00103; B_lectin; 1. SWART; SW00181; EGF; 1.
   Slocus_glycop.
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es 118; Conser
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562
658
128
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473
534
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SIGNAL
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Homo sapiens (
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P51617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 GLVLGFSKSTFTYE--ELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLE--LHLHGEG
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74; Mismatches 211; Indels 134; Gaps
                                                                                                                                                                                                                                                                                       Reichwald K., Kioschis P., Rosenthal A., Platzer M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KINASE ASSOCIATES WI
THE IL-1 RECEPTOR IL1-R-1. THIS ASSOCIATION IS RAPID AND IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: SEEMS TO BE UBLOUITOUS, ALTHOUGH PRESENT SMALL AMOUNTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION OF THE KINASE.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
Cao Z., Henzel W.J., Gao X.; "IRAK: a kinase associated with the interleukin-1 receptor."; Science 271:1128-1131(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: AN EXTENSIVE PHOSPHORXLATION OF IRAK OCCURS AFTER ASSOCIATION WITH ILL-R-1, THIS STEP COULD BE LINKED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000488; Death.
InterPro; IPR000715; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002590; Ser_thr_pkinase.
Pfam; Pr00069; pkinase; 1.
Pr00m; Pr00501; Buk_pkinase; 1.
Pr050m; Pr00107; Pr07EIN_KINASE_ATP; 1.
PR05ITE; PS00107; PR07EIN_KINASE_ATP; 1.
PR05ITE; PS00101; PR07EIN_KINASE_DOM; 1.
ITRNSferase; Serine/threonine-protein kinase; ATP-binding.
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                                                                                                                                                              Platzer M., Bauer D., Drescher B.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F -> S (IN REF. 1).
S -> L (IN REF. 1).
A7ADED75D3A3981D CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF030876, AAC08756.1; -. EMBL, AF031075; AAF21636.1; -. Genew; HGNC:6112; IRAK1.
MIM, 300283; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226
239
338
196
532
5532
S 5536 MW;
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                    RFAGSSPSQSSWVARTQTVRGTLAXLPEEXIKTGRLAVDIDTFSFGVVVLETLAGQRAVK 425
RPIMEWSTRIKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKI- 423
                                                                                                                                                                                   THGARTKYLKD-LVE-----EEAEFAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHL 478
                                                                                                                                                                                                                                                                                               -- DYDSSQYNEDMKKFRKMALGTQEYNAT 603
                                                                                                                                                                                                                                                                                                                           535 ASCIPPSPQENSTVSSTGRAHSGAAPWQPLAAPSGASAQAAEQLQRGPNQPVESDE--SL 592
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                                                                                                                                                                                                                                                    479 DPRPGPCPPELGLGJGQLACCCLHRRAKRRPPMTQVYERLE---KLQAVVAGV-PGHSEA
                                                                                                                                               --DANNVYVDDSLVDWARPILINRASEQGDFEGLADAKMNNGYDREEMARWRA-----
                                                                                                                                                                                                                         ---CAAACVRHSARRPRMSQIVRALEGNVSLSDLNEGMRPGQSNV
                                                                         ---ASDINTHVSTR---VMGTFGYLAPEYAASGKLTEKSDWFSFGVVLLELITGRRPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL PRELIMINARY SEQUENCE FROM N.A.
MEDLINE=91017504; PubMed=1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-: FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Glycosylated polyproline II rods-with-kinks as a structural motif plant hydroxyproline-rich glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                               GEYSNPTSDYGLYPS------GSSSEGQTTREMEMGKIKRTGQGYSGP 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FPQ6; Q03927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21159092; PubMed=11258910;
Ferris P.J., Weessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                   GGLSAALRSWHLTPSCPLDPAPLREAGCPOGDTAGESSWG------SGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF309494; AAG45420.1; -
EMBL; M58496; AAA69706.1; ALT_SEQ.
GlycoSuiteDB; Q9FPQ6; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                             --SYEGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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SEQUENCE FROM N.A.
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365
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InterPro; IPR002965; P\_rich\_extensn.
InterPro; IPR003882; Pistil\_extensin.

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                                                                                                                                                                                                                           5 PSPGTGS--PPSPPSNSTTTTPPPASAPPTTPSSPPPPSTIPTSPPPSSRSTPSAP---
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-cv. Columbia; IISSUB-Green siliques;
MEDLINE=9403320; PubMed=8219075;
Valon C., Smalle J., Goodman H.M., Giraudat J.;
"Characterization of an Arabidopsis thaliana gene (TMKL1) encoding a putative transmembrane protein with an unusual Kinase-like domain.";
Plant Mol. Biol. 23:415-421(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia; MEDLINE-20363099; PubHed=10907853; Raneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.; Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4.251,695 bp regions covered by 90 Pl, TAC and BAC clones.";
                                                                     49 X 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                     78;
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-!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- SIMILARITY: TO PROTEIN KINASES IN THE C-TERMINUS, BUT DOES |
SEEM TO HAVE CONSERVED A KINASE ACTIVITY.
-!- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
                                            POTENTIAL.
VEGETATIVE CELL WALL PROTEIN GP1
                                                                                                                                                                    12.6%; Score 434; DB 1; Length 555; 36.9%; Pred. No. 3.4e-10;
                                                                                                                                                                                                  Indels
                                                                                                                                           6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 PKAPSPPRQP-PPPPPPFMSSSGGSDYSDRPVLPPPSP 252
                                                                                                                                                                                                                                                                                                                                                                  297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
14-Unitive Achase-like protein TMKL1 precursor.
TMKL1 OR AT3624660 OR MSD24.3.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       674 AA
                                                                                                                                                                               36.9%; Pred. ...
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PR01217; PRICHEXIENSN. PR01218; PSTLEXIENSIN.
                              Signal.
                                                                                                                                          54219
                                                                                                                                                                                  Local Similarior
des 103; Conservative
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                                                      555
339
279
399
455
493
                           Glycoprotein; Repeat; SIGNAL 1 2
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493. 4
555 AA;
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                                                                                                                          CARBOHYD
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                                                                                               CARBOHYD
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PRINTS;
                PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFEGNSPSLCGLPLKPCLGSSRLSPGAVAGLVIGLMSGAVVVASLLIGYLQNKKRKSSIE 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 NLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEWEIISRVHHRHLVSL-VGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 CIAGAKRILVYEFYPNNNLE--LHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IHRDIKASNILIDFKFEAKVADFGLAKIASDINTHVSTRVMGTFGYLAFEYAASGKLTEK
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                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN_KINASE_DOM; 1.
mbrane; Glycoprotein; Signal; Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUTATIVE KINASE-LIKE PROTEIN TMKL1.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC.
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26.8%; Pred. No. 6
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N-LINKED
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LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transmembrane;
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PROSIZE; PS50011; PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
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Best Local Similarity
Matches 129; Conserv
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CARBOHYD
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RA Adams M.D., Celniker S.E., 1501 R.B., Evans C.A., Gocayne J.D., Rabintar-2019-2005; "Unbace-10/31132; RA Adams M.D., Celniker S.E., Richards S., Rabburner M., Henderson S.N., Sucton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Wan K.B., Doyle C., Baxter E.G., Fell G., Nelson C.R., Millos G.L.G., Man R.H., Doyle C., Baxter E.G., Fell G., Nelson C.R., Millos G.L.G., Man R.H., Borle B.G., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ball J. Barn M. Baxu M. Baxn M. Marny M. Gong F., Gorrell J. H., Gu Z., Guan P., Harris M. J. Alali M., Kallush F. Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Bulli M., Kallush F. Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Bulli M., Kallush F. Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Mullshina N.Y., Morariz S., Linang Y., Lin X., Mattei B., Mcrhosh T.C., Mcris S., Linang Y., Lin X., Mattei B., Mcrhosh T.C., Morris J., Wosherson D.L., Mount S.M., Mulphy B., Murphy L., Murphy B., Murphy L., Murphy B., Murphy L., Murphy B., Murphy L., Murphy B., Warphy B., Warp
                                            557 SDVIAFGILLLEILMGKKPGKSGRNGNEFVDLPSLVK-AAVLEETTMEVFDLEAMKGIRS
                                                                                         511 -MINGIDREEMARMYACAAACVRHSARRPRMSQIVRALEGINVSLSDLNEGMRP-GQSNV
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SDVFSFGVVLLELITGRRPVDA---NNVYVD-DSLVDWARPLLNRASEQGDFEGLADAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shelton C.A., Wasserman S.A.; Pelle anodes a protein Kinase required to establish dorsoventral polarity in the brosophila embryo."; Cell 72:515-52(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Sukaryota; Metazog, Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                 00552; 09VB57; 01-00T-1994 (Rel. 30, Created) 01-00T-1994 (Rel. 30, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Probable serine/threonine-protein Kinase pelle (EC 2.7.1.37). PLL OR CG5974.
                                                                                                                         616 PMEEG----LVHALKLAMGCCAPVTTVRPSMEEVVKQLEEN-
                                                                                                                                                                                                                                                                                                                                                       501 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MUTAGENES:
MEDLINE-93177834; PubMed-8440018;
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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620 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 T-----FIYEELARAINGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGS-- 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 -GQGEREFQA---EVELISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 IDQKAYELQQSYNELKYLNSIRHDNTIALYGYSIKGGRPCLVYQLAKGGSLEARLRAHKA 308
                                                 IN COMPLEX WITH TUBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 PPSDHVVTSLPPPPRAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKS
                                                                                                                FUNCTION: RECIPED FOR THE NUCLEAR IMPORT OF THE DORSAL PROTEIN WHICH ESTABLISHES DORSOVENTRAL POLARITY IN DRGSCPHILA EMBRYOS. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. SUBUNIT: Interacts with Tube through their respective N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRSVPTISELRAAPDSSAKVNNGPPFPSSSGVSNSNNNRTSTTATEEIPSLESLGNIHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20055599; PubMed=10589682;
Xiao T., Towb P., Wasserman S.A., Sprang S.R.;
"Three-dimensional structure of a complex between the death domains of Pelle and Tube.";
Cell 99:545-555(1999).
                                                                                                                                                                       -!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE WITH HIGHEST LEVELS IN 0-3 HOUR-OLD EMBRYOS AND ADULT FEMALES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00108; PROTEIN_XINASE_ST; 1,
PROSITE; PS50011; PROTEIN_XINASE_DOM; 1,
PROSITE; PS50017; DEATH_DOMAIN; 1
Transferase; Serine/threonine-protein kinase; AIP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4B29E2B40ACB81A8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D->A: REDUCED ACTIVITY.
A->E: REDUCED ACTIVITY.
Myers E.F., Rubin G.M., Venter J.C.; sequence of Drcsophila melanogaster.";
                                                CRYSTALLOGRAPHY (2.00 ANGSTROMS) OF 26-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 357.5; DB 1
Pred. No. 9.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEATH.
PROTEIN KINASE.
ATP (BY SIMILAR:
ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Mismatches
                                                                                                                                                                                                            PELLE SUBFAMILY.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM: 1.
                                                                                                                                                                                                                                                                                                                                                     EMBL, A5003760; AAF56686.1; -. PTR: A4775; A45775
PDB; 1D22; 29-NCW-99.
FlyBase; FBG00010441; pll.
InterPro; IPR000488; Death.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000001; Euk_pkinase; 1.
SM00005; DEATH; 1.
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                       Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase; 1.
Pfam; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                            EMBL; L08476; AAA28750.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 114; Conservative
                                                                                                                                                                  DEATH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
 Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-structure.
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MUTAGEN
MUTAGEN
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NP_BIND
BINDING
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                                                X-RAY
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                                                                                                          422 K---IASDINTHVSTRVMGTFGYLAPBYAASGKLTEKSDVFSFGVVELELITGRRPVDAN 478
      421
                                 ----RVPENETKKNLLDYVKQQWRQNRMELLEKHLAAPMGKELDMCM 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: EXTRACEILUIAR MALTIX.
PIN: EXTENSING CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE
SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
GLYCOSYLATED.
----PTMEWSTRLKIALGSAKGLSYLHEDCNPKTIHRDIKASNILIDFKFEAKVADFGLA
                                                                                                                                                                    REGPKSLDAVVEVN-KVFGTKIYLPPEFRNFRQLSTGVDVYSFGIVLLEVFIGRQVTD--
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2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco).
Wataryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Extensin precursor (Cell Wall hydroxyproline-rich glycoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoprotein gene in lateral root initiation.";
Genes Dev. 3:1639-1646(1989).
-!- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY
THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reller B., Lamb C.J.;
"Specific expression of a novel cell wall hydroxyproline-rich"
                                                                                                                                                                                                                             479 NVYVDDSLVDWARPLLNRASEQGDFEGLAD-AKMNNGYDREEMAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S06733; S06733.

Repeat; Cell wall; Glycoprotein; Signal; Structural protein; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS THE SER-PRO(4) REPEATS
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Pred. No. 2.1e-07;
9; Mismatches 65; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-cv. Xanthi; TISSUE-Leaf;
MEDLINE-90128263; PubMed-2612909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65406 MW;
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Matches 97; Conservative
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4 APSPCTGSPPSPPSNSTITTPPPASAPPTTTPSSPPPPSTIPTSPPPSSRSTPSAPP-S 62	347 SPPPVYSPPPPSKSPPPPTYLPPPPSSPPPPSSSPPPPTYEQSPPPPAYS 400	63 PPTPSTPGSPPPIPQPSPPAPTTPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPS 122	401 PPLPAPPTYSPPPPTYSPPPTAQPPPLPFTYSPPPPAYSPPPPTYYSPPPPT 454	123 -SPSPPSPSSDGLSTGVVVGLAIGGVALLVIVTEJCLLCKKKRRDEEDAYYVPPPPP 179	×	GGQQQQWRQQN	YSPPPPAYSPPPPSP-IXSPPPDQVQPLPPFSSPPPRRIHLDPPP 516	232 FMSSSGGSDYSDRPVLPPPSP 252	517 ERQPRPPTPTYGQPPSP 533
4	347	63	401	123	455	180	472	232	517
QY	qq	Ωλ	옆	Δ.	g	ZZ.	qq	QY	qq

Search completed: July 2, 2003, 15:22:46 Job time: 28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 15:16:13 ; Search time 73 Seconds (without alignments) 1181.002 Million cell updates/sec July Run on:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST.....REMEMGKIKRTGQGYSGPSL 647 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapert 9.5 Searched:

908470 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SIDS2/goddata/geneseq/geneseqp-embl/AA1991.bAT: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Brassica napus PER	Herbiridally activ	Arabidonese theles	Horbioidad	derivation delia	Protein encoded by	Herbicidally activ	Herbicidally activ	protein enough hy	Herbicidally activ	Herbicidally activ
SUMMARIES			ID			ABB92424	AAG15453	ABB92231	1000	AAB/470/	ABB91790	ABB91291	AAB74208	ABB93235	ABB92360
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	<sub>O</sub> M <sup>2</sup>	Query	re Match Length DB I	1 1 1 1 1 1 1 1 1	9.66	85.0	65.5	90.9		0,00	50.6	50,1	48.9	48.9	48.8
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New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen

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1569.5 1515.5 1459.5 1415.5 1415.5	8889 8888 13698 8868 868 868 878 878 878 878 878 878 8	780.5 775.5 775.7 774 773 773	9	757 757 754.5 750 750 745
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## ALIGNMENTS

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Proline-rich extensin-like receptor kinase; PERK; resistance;
             AAB74205 standard; protein; 647 AA.
                                                        Brassica napus PERK1 protein.
                                                                                                                                       18-AUG-2000; 2000WO-CA00966.
                                                                                                                                                     990S-0149466.
990S-0159122.
                                          (first entry)
                                                                                                                                                                                                                WPI; 2001-244305/25.
                                                                                                                                                                                                 Goring D, Silva N;
                                                                                                                                                                           (GORI/) GORING D.
(SILV/) SILVA N.
                                                                                            Brassica napus.
                                                                                                          WO200114563-A1.
                                         17-MAY-2001
                                                                                                                                                    19-AUG-1999;
13-CCT-1999;
                                                                                                                         01-MAR-2001.
                            AAB74205;
                                                                             plant.
RESULT 1
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Herbicidally active polypeptide SEQ ID NO

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  producing transgenic plants with increased wounding
                                                                                                                                                                                                                         PSSPSPPSPSSDGLSTGWWGIAIGGWALLVIWTLICLLCKKKRRRDEEDAYYVPPPPP
                                                                                                                                                                                                           MSSAPSPGTGSPPSPPSNSTTTTPPPASAPPPTTPSSPPPSTTPTSPPPSSRSTPSAPP
                                                                                                                                                                                                                                                   PSPPTPSTPGSPPPLPQPSPPAPTTPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRP
                                                                                                                                                                                                                                                                                                                                    GPKAGGPYGGQQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPFMSSSGGSD
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                                                                                                                                                                                                                                                                                                       AVKOLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKIASDINTHVSTRVMGTFGTLAPEYAASGKLIEKSDVFSFGVVLLELITGRRPVDANNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVDDSLVDWARPLLKRASEQGDFEGLADAKHNNCYDREEMARWYACAAACVRHSARRRPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                               The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and parhogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide
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                                                                                                                                                                         647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3440; DB 22;
Pred. No. 4e-L81;
0; Mismatches 2;
                                Fig 1; 91pp; English.
                                                                                                                                                                     99.68;
99.78;
                                                                                                                                                                           Local Similarity 99.7
les 645; Conservative
            resistance
                                                                                                                          function directly.
                                                                                                                                                647 AA;
  ğ
            pathogen
 resistance,
                             Claim 30;
                                                                                                                                                Seguence
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The invention relates to identifying target proteins comprising aligning and comparing nucleic acid or mains acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similiar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSSAPSPGT---GSPPSPSPSTTTTPPPA--SAPPTTPSSPPP-PSTIPTSPPPSSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 TPSARPPSPPTPSTPGSPPPLPQPSPPAPTTPGSPPAPVTPPT-RNPPSVPGPPSNPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSTAPSPGTTPSPSPPSPPTNSTTTTPPPAASSPPPTTTPSSPPSPSPSTNSTSPPPSSPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPP-FMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVELISRVHHRHLVSLVGYCIAGAKRLLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEFVPNNNLELALAGGGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 652;
                                                                                                                                                                                                                                                                                                                                             Claim 5; SEQ ID NO 1635; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%; Score 2936.5; DB 2:87.0%; Pred. No. 1.7e-153;
                         Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                28-AUG-2001; 2001WO-EP09892.
                                                                                                                                     28-AUG-2001; 2001WO-EP09892.
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                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful as herbicides.
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                                                                                                                                                                                                                        Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 AA;
                                                                                                                                                                                             (FARB ) BAYER AG
                                                                                WO200210210-A2
                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574;
                                                                                                                                                                                                                       Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Protein;

ABB92424 ABB92424;

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(first entry)

31-MAY-2002

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    413 DEKFEBAKVADFGLAKIASDINIHVSTRVMGIFGYLAPEYAASGKLIEKSDVFSFGVVLLE 472
                  LITGRRPVDANNVYVDDSLVDWARPLLINRASEQGDFEGLADAKMNNGTDREEMARMVACA 527
                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 15711,
                                                                                                                                                     AAG15453 standard; Protein; 544 AA.
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99US-0123180.
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                                                                       55 TPSAPPPSPPTPSTPGSPPPLPQPSPPAPTTPGSPPAPYTPPT-RNPPPSVPGPPSNPSR
                                                                                                                                 PPP-FMSSSGGSBYSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFG
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                               Gaps
                               23;
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          Pred. No. 1.8e-116;
7: Mismatches 40;
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83.3%; PLC
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                             Conservative
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              Best Local Similarity
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Length 544;

Score 2260.5; DB 21;

65.58;

Query Match

(first entry)

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Proline-rich extensin-like receptor kinase; PERK; resistance;
                          Protein encoded by Arabidopsis gene #2.
                                                                                                                                           18-AUG-2000; 2000WO-CA00966
                                                                              Arabidopsis thaliana
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                   The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
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                                                                                                                                                   DB 23; Length 694;
SEQ ID NO 1632; 261pp + Sequence Listing; English.
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                                                                                                                                                 Score 2093,5; DB 2
Pred. No. 3.2e-107;
7; Mismatches 112;
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99US-0149466.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGDTGGSRSDNPPSSGGSSGGGGGRSNTNTALIVGVLVCGAGLLMIVLIIVCLFRKKKRK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDEEDAYYVPPPPPPPPRAGGP---YGGQQQWRQQNATPPSDHYVTSLPPPPKAPSPPR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLIGOGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQARVEIISRVHHRHLVSLVGYC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPSPGTGSPPSPPSRSTTTTPPPRASAPPTTPSSPPPPSTTPTTPSPPPSSRSTPSAPPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS-----SPSPPSP--SSDG------LSTGVVVGIAIGGVALLVIVTLICLLCKKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 NILGOGGEGTYHKGVLPSGKEVAVKSLKAGSGGGEREFQAEVDIISRVHHRYLVSLVGYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DSFY-----PEPMKGNOYOYYGNNNNNASQNY--PNWHINSQGONOQSTGGWGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 OPPPPPPPPPEMSSSG--GSDYS--DRPVLPPPSPGLVLGFSKSTFTYBELARAINGFSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                            The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic
                                                                                                                                                                                                                                                                                                                                   plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.6%; Score 1748.5; DB 22
56.8%; Pred. No. 2.5e-88;
ive 78; Mismatches 151;
                                                                                                                                                   Examples; Fig 12; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363; Conservative
                                                                                               pathogen resistance
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Best Local Similarity
Matches 363; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         function directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to identifying target proteins (ABB9079C-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with rucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them useful for identifying modulators. The identified modulators are useful as herbicides.
IADGQRMLVYEFVENKTLEYHLHGKNLPVWEFSTRLRIALGAAKGLAYLHEDCHPRIIHR
                                                                        FSFGVVLLELITGRRPVDANNVYVDJSLVDWARPLLNRASEQGDFBGLADAKMNNGYDRE
                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                        OIKASNI LIDFKFEAKVADFGLAKIASDINTHVSTRVMGIFGYLAPEYAASGKLTEKSDV
                                                                                                                      EMARMVACAAACVRHSARRPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDY
                                                                                                                                    Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; SEQ ID NO 1001; 261pp + Sequence Listing; English.
                                                                                                                                                                                     SQTSYNADMKKFRQIALSSQEFPVSDCGTSSNDSRDMG 625
                                                                                                                                                                           51.4
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                                                                                                                                                                      DSSQYNEDMKKFRKMALGTQEY ---NATGEYSNPTSDYG
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 1748.5; DB 56.8%; Pred. No. 2.5e-88; ive 78; Mismatches 151
                                                                                                                                                                                                                                                                                                                                                           agriculture; herbicide,
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                                                                                                                                                                                                                                                                                                                               Herbicidally active polypeptide
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                                                                                                                                                                                                                                                                                                                                                          plant;
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                    PPN-SSNNSPSPPSQGGGGERGNGGNNGGNDTPPSRGSPPS---PPSRSNGDNGGSRSSP
                                             PS-----SPSPPSP--SSDG-----LSTGVVVGIAIGGVALLVIVILICLLCKKKRR
                                                             120 PGDTGGSRSDNPPSSGGSSGGGGGRSNTNTALIYGVLVGAGLLMIVLLIYCLRRKKRRR
                                                                                        RDEEDAYYVPPPPPPPPRAGGP---YGGQQQQWRQQNATPPSDHVVTSLPPPPRAPSPPR
                                                                                                             180 ----DSFY-----PEPMKGNQYQYYGNNNNNNASQNY--PNWHINSQGQNQQSTGGWGG
                                                                                                                                                                                 NILGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYC
                                                                                                                                                                                                                                                                                                                       FSFGVVELELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDRE
                                                                                                                                      223 OPPPPPPPPFMSSSG--GSDYS--DRPVLPPPSPGLVLGFSKSTFIYEELARAINGFSEA
                                                                                                                                                    IAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGESYLHEDCNPKILHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying plant target proteins for herbicidally active compounds, comprishs aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from mon-plant
                                                                                                                                                                                                                                                                                                                                                                                                               DSSQYNEDMKKFRKMALGTQEY---NATGEYSNPTSDYG 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbicidally active polypeptide SEQ ID NO 502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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Gaps

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Similarity

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SAPSPGTGSPPSPPSNSTTTTPPPASAPPPTTPSSFPPPSTIPTSPPPSSRSTPSAPPPS SAPPTNSTSSPERENTNSTISSP---PAPSPERPPQGDSSSSPPDSTSPPAPQADN Arabidopsis gene #3.

(first entry)

99US-0149466.

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Silva

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New proline-rich, extensin-like receptor kinase nucleic acids polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased or pathogen resistance.
                                                                  Proline-rich extensin-like receptor kinase; PERK; resistance;
                                                                                                                                                                  18-AUG-2000; 2000W0-CA00966
                                                                                                  Arabidopsis thaliana
                                                encoded by
                                                                                                                                                                                                                                                                      WPI; 2001-244305/25
                                                                                                                                                                                                                              SILW/) SILVA N.
                                                                                                                       WO200114563-A1
                                                                                                                                                                                                                    (GORI/) GORING
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                           17-MAY-2001
                                                                                                                                                                                                13-0CT-1999;
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                                                                                                                                                                                                                                                    Goring D,
      AAB74208;
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                                       The invention relates to identifying target proteins (ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                              127
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCI-AGAKRLLVYEFVPNNNLE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 LHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFFBAKVAD 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGLAXIASDINIHVSTRVMGTFGYLAPEYAASGKLITEKSDVFSFGVVLLELIIGRRPVDA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            959
                                                                                                                                                                                                                                                                                                                                                   2 SSAPSPGIGSPPSPPSNS--TTTTPPPA-----SAPPPTTPSSPPPPSTIPTSPPP---
                                                                                                                                                                                                                         ENSSDGSSSSSPPPPSDSSQSQSPPP-PSTSPPQQSDNNGNKGNNENNKGNDGSSGDG
                                                                                                                                                                                                                                                                                             GSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSPPSSSDGLSTGVVVGIAIGG
                                                                                                                                                                                                                                                                                                                GNKNMSHTP----PPPSKTSDHSSHSQPRSLAPPTSNSGSNSSSNDGLNIGAVIGLVAAA
                                                                                                                                                                                                                                                                                                                                     VALLVIVTLICLLC---KKKRRRDEEDAYYVPPPPPPPPRAGGPYGGQQQWRQQNATPP
                                                                                                                                                                                                                                                                                                                                                                                             SD---RPVLPPPSPGLVLGFSKSTFTYEELARATWEFSEANLLGQGGFGYVHKGVLPSGK
                                                                                                                                                                                                                                                                                                                                                                                 ----KAPSPPR----SDPPPPPPFMSSSGG-----SDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                         Length 699;
                     261pp + Sequence Listing, English.
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                                                                                                                                                                                            Indels
                                                                                                                                                                     Score 1729; DB 23;
Pred. No. 3.3e-87;
3; Mismatches 167;
                                                                                                                                                                                                                                                      ---SSRSTPSAPPSPPTPSTPGSPPFLPQPSPPAPT-
                                                                                                                                                                                         83;
                                                                                                                                                                    50.1%;
                                                                                                                                                                                          Conservative
                    SEQ ID NO 502;
                                                                                                                                                                               Similarity
                                                                                                                                                 699 AA;
                                                                                                                                                                                     Matches 372;
  organisms
                    Claim 5;
                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 GYVVGIAIGGVALLVIVTLICLLCKKKRRDEEDA----YYVPPPPPPPPRA-G3PYGGQ 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSSAPSPGTGSPPSPSNSTTTTPPPASAPPPTTPSSPPPFSTLPTSPPPSSRSTPSAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VDSSPAPET-SNGTPPSNGTS---PSNESSPPTPPSSPPSS---ISAPPPDISASFSPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TPQDHVV-NMAGQGGGNWGPQQPVSGP-----HSDASNLTGRTAIPSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                 The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                  48.9%; Score 1687; DB 22;
51.8%; Pred. No. 6.3e-85;
iive 87; Mismatches 142;
Examples; Fig 13; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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nes 368; Conserv
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AAB74208 standard; protein; 674

AAB74208 ID AAB7 XX

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GEREFGAEVDIISKVHHRHLVSLVGYCISGGQRLLVYEFIPNNILEFHLEGKGRPVLDWP 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                YVDDSLVDWARPLINRASEZGDFEGLADAKMNNGYDREEMARWYACAAACVRHSARRRPR
                                                                                                                                                                   MSQ-----IVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKK
GEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWS
                                                  ---NPKIIHRDIKASNILIDEKFEAKVADFGL
                                                                                                 AKIASDINTHVSTRVMGTFGTLAPEYAASGKLITEKSDVFSFGVVILLELITGRRPVDANNV
                                                                                                              FRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMGKIKRTGQ
                                                                                                                                                                                                                                                                   SEQ ID NO 2446; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Herbicidally active polypeptide SEQ ID NO 2446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  herbicide
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                                                 TRLKIALGSAKGLSYLHEDC-
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Query Match

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                                                                                   GVVVGIAIGGVALLVIVTLICLLCKKKRRRDEEDA----YYVPPPPPPPPAA-GGPYGGQ
                                                                                                                                                                                                            229 -----TPQDHVV-NWAGQGGGNWGPQQPVSGP-----HSDASNLTGRTAIPSPQ
                                                                                                                                                                                                                                                    -AATLGENQSTFTIDELSIATEGFAQSNLLGGGGGTVHKGVLPSGKEVAVKSLKLGSG
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                             1 MSSAPSPGTGSPPSPSSNSTTTTPPPASAPPPTTPSSPPPPSTIPTSPPPSSRSTPSAPP
                                                                                                              --SWEGPPSNPSR---EGGSPRPPSSPSPPSPSSDGLST
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                                                                     PSPPT----PSTPGSPPPL----PQ----PSPPAP--TTPGSPPA-PVTP-
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           Indels
 Pred. No. 6.3e-85;
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51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TPPTANEPPSVPGPPSNPSREGGSPRPPSSPSPSSSD 132
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                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                           Length 700;
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                                                                                                                                                                                                                                                                                                                                                                                                                              7 PENSPESPTEPSPSSSDNQQQSSPPPSDSSSPSPPAPPPEDSSNGSPQP-
                                                                                                                                                            SEQ ID NO 1571; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                   146;
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Pred. No. le-84;
; Mismatches 14
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              (FARB ) BAYER
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Matches 353; (
                                       Tietjen X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to identifying target proteins (ABB94016) for herbicidally active compounds, comprising algining and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant are useful for identifying modulators. The identified modulators are subscited as herbicides.
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582 QYNEDMKKFRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMGKIKRTG 639
                                                            ---- SIRRGG 688
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                                   DB 23;
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53.2%; Pred. No. 1.3e
ive 45; Mismatches
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Best Local Simi
Matches 345;
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204 VANCIANGSERGEREPARTH		W-1.	Query Match
360 Incorrendential in [11] [11] [11] [11] [11] [11] [11] [11			Matches
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420 LAKIASDTWINVSTRVMGTPCKIAPETAASGKITEKSDVFSFCVULELITGREPADANN 480 VYVDADDTWHYSTRVMGTPCKIAPETAASGKITEKSDVFSFCVULELITGREPADANN 480 VYADADTWHYSTRVMGTPCKIAPETAASGKITEKSDVFSFCVULLELITGREPADANN 480 VYADADSLUWARPLILAASGCOFFGLADKIANEETSPREBARNACAAACVREARRE 540 RAGQIVRALEGNVSIEDINGITPGRANNOCAACVREARRE 540 RAGGIVRALEGNVSIEDINGITPGRANNOCAACVREARRE 540 RAGGIVRALEGNVSIEDINGITPGRANNOCAACVREARRE 541 [11] [11] [11] [11] [11] [11] [11] [1		Ö	Db
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sequences are selected. The polymetrian is most smitter into the are useful for identifying modulators. The identified modulators are	E	XXX	x W Herbicida X

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                                                                                                                                                     .----SPPTP----STPGSP 72
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                                                                                       --SAPPPTTPSSPPPPSTI
                                                                                                                                                                                                                   -----SPPAPTIPG-SPPAPVIPPTRN-----PPPSV
                                                                                                                                                                                                                                                                         5 P--GPPSNPSREGGSPRPPSSPSSPSSPGLSTGVVVGIAIGGVALLVIVILICLLCKK
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                                                                                                                                                                                                                                                                                                                                                                                                                         3 ------VMGSGQTHFTYE
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                        th 43.9%; Score 1515.5; DB 23; Length 710; Similarity 46.2%; Pred. No. 1.7e-75; Conservative 81; Mismatches 158; Indels 149; Gaps
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710 AA;
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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
      GLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKIASDINTHVSTRVMGTFGYL
                        APEYAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGD
                                                                                                     544 APEYASSGKLITEKSDVFSFGVVLLELITGRKPVDTSQPLGDESLVEWARPLISHAIETEE
                                                                                                                                    FEGLADAKMINGYDREEMARMVACAAACVRHSARRPPRMSQIVRALEGNVSLSDLNEGMR
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                                                                                                                                                                                                    563 PGOSNVYSSYGGSTDYDSSQYNEDMKKFRKMALGTQEYN 601
                                                                                                                                                                                                                        42.2%; Score 1456; DB 23;
46.4%; Pred. No. 3e-72;
ive 87; Mismatches 158;
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Watches 306; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EILVPGSNNPSQNNPTLRPPLDAPNSTNNSGIGTGAVVGISVAVALVVFTLFGIFVWCLR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIYEELARAINGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEI 322
                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying target proteins (ABB90790-ABB9016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them execused if the polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
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(4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVANGAPPPLPKFPESSSPPPQPVIPSPPFSTSPPPQPVIPSPPSASPPPALVPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSSAP----SPGTGSPPSPSNSTT-TTPPPASAP-PPTTP---SSPPPPSTTPTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATTPVQPPVSNSPPVTSPPPDLNNATSPATPPPVTSPLPPSAPPPNRAPPPPVTTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SPPSPSSDGLSTGVVVGIRIGGVALLVIVTLICLLCKKKRRRDEEDAYYVPPPPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LGESKST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ERPTQSPPPPSPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAGGPYGGQQQWRQQNATPPSDHVVTSLPPPPK--APSPPRQPPPPPFMS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                 proteins for herbicidally active compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred, No. 2e-72;
); Mismatches 127; Indels 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 708;
                                                                                                                                                                                                                                                                                                              ID NO 715; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPSSRSTP-----SAPPPSPPTPSTPGSPPLPQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1459.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
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                                                               28-AUG-2001; 2001WO-EP09892,
                                                                                              28-AUG-2001; 20:01WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity ... hes 317; Conservative
                                                                                                                                                                                                                            Identifying plant target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful as herbicides.
                                                                                                                                                                Weidler
                                                                                                                                                                                              WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -Sagsadscl
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                                                                                                                               (FARB ) BAYER AG.
WO200210210-A2.
                                                                                                                                                                                                                                                                                                              SEQ
                              07-FEB-2002
                                                                                                                                                                Tietjen K,
                                                                                                                                                                                                                                                                                                             Claim 5;
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147 129 207 159 267 202 325 262 382 471

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591

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SLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMYACAAACYRHSARRRPRMSQI 544
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     polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding
                                                                                                                                                                                                                                                                                                                                                                                         ----SSDGLSTG-----VYVGIAIGGVALLVITLICLL
                                                                                                                                                                                                                                                                                                                                                                                                                                               208 PSSGPVVSPSLTSPSKGTPTPNQGNGDGGGGGGGGGGKTMVGMAVAGPAIMALIGVVFLV
                                                                                                                                                                                                                                                                                                 29 NSALPPVDSSPPSPPADSSSTPPLSEPSTPPDSQLPPLPSILPPLTDSPPPPSDSSPPV
                                                                                                                                                                                                                                                                                                                          PSTIPTSPPPSSRSTPSAP----PPSPPTPSTPGSPPP----LPQPSPPA----PTTP
                                                                                                                                                                                                                                                                                                                                                  DST-PSPPPPTSNESPSPPEDSETPPAPPNESNDNNPPPSQDLQSPPPSSPSPNVGPTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 RRKKKR--NIDSYNHSQYLPHPHFSVKSDGFLYGQDPGKGYSSGPNGSMYNNSQQQQSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKKKRRRDEEDAY----YVPPP------PPPGPKAGGPYGGQQQWRQQNATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSDHVVTSLPPPPKAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 GNSYGTAG- ----SGYPHHQ------MOSSGTPD-----SAILGSGQTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTYBELARATNGFSEANELGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 SDINTHVSTRVMGTFGYLAPBYAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDD
                                                                           The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                       41.0%; Score 1415.5; DB 22
43.4%; Pred. No. 5.4e-70;
ive 93; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSTLHEDCNPKIIHRDIKASNILIDEKFEAK----
                                                                                                                                                                                                                                                                         SSAPSPGIGSPPSPSNSTIT-----TPPPAS-
                                                     Examples; Fig 11; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYS-----GNYSAKSSSD 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYSNPTSDYGLYPSGSSSE 623
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                                                                                                                                                                                                                                   Best_Local Similarity 43.4
Matches 321; Conservative
                               or pathogen resistance
                                                                                                                                                                                              731 AA;
                                                                                                                                                                      function directly.
                                                                                                                                                                                               Sequence
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                     QTVSPPPPPDASPSPAPTITANPPRKPSPSPPGETPSPPGETPSPPKPSPSTFTFTTTS 170
                                                                                               SPSSDGLSTG--VVVGLAIGGVALLVIVTLICLLCKKKKRRDEEDAYYVPPPPPPGFKAG 185
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                                                 -----PPSVPGP-----PSNPSREGGSPRPPSSPSPP 127
                                                                                                                                                                                                                                                                                                                                                                                                                          IVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDFDSSQXNEDMKKFRKMALGTQEYNA 602
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                                                                                                                                                                                                                                                                                                                     GPYGGQQQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPPPSSSGGSDYSDRP
                                                                                                                                                                                                   VLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQL
                                                                                                                                                                                                                   KVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHIHGEGR
                                                                                                                                                                                                                                                                     PTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKIAS
                                                                                                                                                                                                                                                                                                                                                                      --DINTHVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVDANNYYVD
                                                                                                                                                                               -----MRSHSGSDY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proline-rich extensin-like receptor kinase; PERK; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Arabidopsis gene #1.
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| VYRALDILEEATDITNGMRPGQSQV----
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dSbdlbdlddSd----
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                                               PPAP----VIPPIRNP--
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(SILV/) SILVA N.
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13-OCT-1999;
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Search completed: July 2, 2003, 15:22:14 Job time: 76 secs

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GenCore version 5.1.6
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2, 2003, 14:57:12; Search time 18 Seconds (without alignments) 1057.591 Million cell updates/sec July Run on:

Title;

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST......REMEMGKIKRTGQGYSGPSL Perfect score: Sequence:

647

BLOSUM62 Gapop 10.0 Gapext 0.5 Scoring table:

262574 segs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Issued\_Patents\_AA:\* Database :

1: /cgg2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Prec. Wo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMBLEDTEC

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Result	Score	Query Match	Length	DB	ID	Description
-	754 5	21 0	0.00			1.
1 0	1 1	7.1.0	000	*	000	Sequence 76, Appl
7	/30	ZT.3	630	4	-228-	71,
m	703.5	20.4	707	4	986	2
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Ŋ	604.5	17.5	1196	4		
9	593	17.2	903	4	-09-228-	
7	579.5	16.8	980	7	-6F4-80-	
ю	575	16.7		7	-08-255-628-	5
σ	572.5	16.6		7	-08-473-	ì
10	572	16.6		Н	-07-717-	ì
11	566.5	16.4		7	-09	, Q
12	560.5	16.2		4	-09-228-	Sequence 77 appl
13	552	16.0		7	-08-473-553A-	-
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15	545	15.8	544	N	-587	1 5
16	543	15.7	655	7	- 1	20
17	539.5	15.6	857	Н	US-07-717-3315-3	2
18	525	15.2	666	7	-473-	, tr
19	206	14.7	712	Н	US-08-587-889-2	Segmence 2. Appli
20	206	14.7	712	C	US-08-980-060-5	'n
21	506	•	712	4	US-09-307-185-5	'n
22	206	14.7	712	Ŋ	PCI-US96-09193-2	'n
23	495		629	4	-228-986-	75
77		•	739	뼥	US-09-503-922-I	H
25		13.2	711	4	US-09-228-986-79	Sequence 79, Appl
26			069	4	US-09-228-986-69	69
27	393.5	11.4	1025	7	US-08-567-375-4	

Sequence 4. Appli	4		seducince o, Appli	Sequence 6, Appli	73,	, C.	Ġ	Ċ,	Sequence 4. Appli		-4		· (-	32	5	Seguence 65. Anni	, 15	,
US-08-587-6804-4	US-08-475-8918-4	712-08-080-050-6	0-000 000 000	US-09-307-185-6	US-09-228-986-73	US-08-475-891A-2	US-08-567-375-2	US-08-587-680A-2	US-08-445-640-4	US-08-170-558-4	US-08-447-314-4	US-08-445-461-4	US-08-336-343A-2	US-08-642-255-32	US-07-609-716-65	US-08-475-411A-65	US-08-478-029A-65	TTC-00-500-5460-6
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11.4	10.7	10		TO.6	10.6	10.2	10.2	10.2	10.0	10.0	10.0	10.0	6.6	9.6	9.6	9.6	9.6	c o
393.5	368	367.5		367.5	357.5	351	351	351	347	347	347	347	341	331.5	331.5	331.5	331.5	329 5
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/LO20
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 DAYYVPPP----PPPGPKAGGPYGGQQQQWRQQNAIPPSDHVVISLPPPPKAPSPPRQPP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 LVYEFTPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNI 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                Indels 115;
                                                                                                                                                                                                                                                                                                                                                Length 968;
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35.3%; Pred. No. 1.2e-35;
ive 89; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 -ALELSRPFASWAPSGKDSGGAPQLKGARW-----
RESULT 1
US-09-228-986-76
; Sequence 76, Application US/09228986
; Patent No. 6359198
                                                                                                                                                                                                                                                                                      GRGANISM: Eucalyptus grandis
US-09-228-986-76
                                                                                                                                                                                                                                                                                                                                            Query Match 21.9
Best Local Similarity 35.3
Matches 184; Conservative
                                                                                                                                                                                                                                       SEQ ID NO 76
                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Strabala, IImothy
APPLICANT: Strabala, IImothy
APPLICANT: Newenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 71
LENGTH: 630
MLELITAKQPIEKGKYVVRE----IRTAMDKNDQ--DYYGVREMMDPSMRSMGY-LVGF 876
                                              PAPVTPPTRNPPPSVPGPP---SNPSREGGSPRPPSSPSPPSPSDGLSTGVVVGIAIGG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 VHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLE--LHLHGEGRPTMEWSTRLKIALGSAKG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 630;
                                                                                  581 SQ-----YNEDMKKFRKMALGTQEYNATGEYSNPTSDYGL 615
                                                                                                  125;
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8.5e-35;
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37.2%; Pred. No. 8.6e
.ive 68; Mismatches
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Patent No. 6359198
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Patent No. 6359198
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.2%
Matches 175; Conservative
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US-09-228-986-71
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US-09-228-986-71
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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
ITILE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
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Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/A1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DAIE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 638
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 G--SGQSEREFQAEVELISRVHHRHLYSLYGYCIAGAKRLLYYEFVPNNNL--ELHLHGE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 GRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKI 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 ASDINTHVSTRYMGIFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVD 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 QSLVRWAIPQLH-----DIDALAKMYDPALKGSYPAKSLSRFADIIALCIQPEPEFRPP 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 WRQQNATP--PSDHVVTSLPPPPRAPSPPRQPPPPPPPPPRSSSG-----GSDTSDRPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 STLSLQRPEDFLDAVSNISRLHHPNITBLYGYCTEHEQYLLYYEYFDNGSLYDYLHMADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSLVDWARPLLNRASEQGDFEGLA---DAKMNNGYDREEMARWVACAAACVRHSARRPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 SGGAIVGIIFAVILTVVAAILGVIIYARKSPRREQD-
                                                                                                          CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.0%
Matches 178; Conservative
                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-80
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US-09-228-986-74
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TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 FIYEELARATHGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEI 322
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                                                                                             446 YAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEG
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                                                                                                                                                       506 LADAKMNIGYDRE-----EMARMVACAAACVRHSARRPRMSQI----
                                                                                                                Length 903;
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APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.2%; Score 593; DB 4; Lv
44.9%; Pred. No. 1.7e-26;
tive 52; Mismatches 99;
                                                                                                                                                                                                                                       -NVSLSDLNEG 560
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CURRENT FILING DATE: 1999-01-12
NUMBER OF ERQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/09228986
Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08473553A Patent No. 5859338
                                                                                                                                                                                                                    -----VRALEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Eucalyptus grandis
US-09-228-986-78
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                                                                                                                                                                                                                                                            473
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                                                                                                                                                                                                                                                                                                                                                                 107 PP----SNPSREGGSPRPPSSPSPSPSSDGL----STGVVVGIALGGVALLVIVTLIC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L------LCKKKRRDEEDAYYVPPPPPPGPKAGGPGGQQQQWRQQNATPPSDHVV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLPPPPKAPSPPRQPPPPPPPPPKSSSGGSDYSDRPVLPPPSPGLWLGFSKSTFTYEEL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 ARAINGFSEANLLGQGGFGTVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHH 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHLVSLVGYCIAGAKRLLVYEFVPNNNLE--LHLHGEGRPTMEWSTRLKIALGSAKGESY 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807 IFGLILVGREMRKRRKKEAELEMYA----EGHGNSGDRTANNTNWKLTGVKEALSINL 861
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                                                                                                                      487 VDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMVACAAACVRHSARRPRMSQIVR
                                                                                                    254 IVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYHKGVLPSGKEVAVKQLKVGS-GQG
                                                                                                                                                               EREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLE--LHLHGEGRPTWEW
                                                                                                                                                                                  VSTRVMGTFGYLAPEYAASGKLITEKSDVFSFGVVLLELITGRRPVD----ANNVYVDDSL
                                                                                                                                                                                                                                                                                                    Gaps
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                                              Length 638;
                                                                           68; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          547 ALEGNVSLSDINEGMRPGQSNVYS----SYGGSTDYDSS 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --
                                             Score 678; DB 4;
Pred. No. 1.7e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08881766
Patent No. 6245969
GERRAL INFORMATION:
APPLICANT: Chong, Joane
APPLICANT: Li, Jianming
TILLE OF INVANION: Receptor Kinase BINI
FILE REFERENCE: 07251/022001
CURRENT APPLICATION NUMBER: US/08/881,706
CURRENT FILING DATE: 1997-06-24
CURRENT FILING DATE: 1997-06-24
SOFTWARE: PatentIn Ver. 2.0
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43.18;
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                                        Query Match
Best Local Similarity 43.1%
Matches 147; Conservative
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Pinus radiata
; ORGANISM: Pi:
US-09-228-986-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1196
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Best Local Simi
Matches 157;
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US-08-881-706-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593 PLGG---OFLVFNETSFAGNTYLCLPHRVSCPIRPGQT-----SDHNHTAL 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 FSPSRIVITVIAAITGLILISVAIRQMNKKKNQKSLAWKLTAFQKLDFKSEDVLEC---L 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693 KEENLIGKGGSGIVYRGSMPNNVDVAIKRL-VGRGTGRSDEGFTAELQTLGRIRHRHIVR 751
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ilarity 34.8%; Pred. NO. 1.1e-55;
Conservative 65; Mismatches 134; Indels 61
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                                                    Albritton & Herbert
Suite 3400
TITLE OF INVENTION: Transformed Plants, and Proteins
                                                                                 CITY: San Francisco
CUNTRY: United States
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
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TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPKAX: (415) 398-3249
TELEKX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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....erR: US/08/473,553A.
06-JUN-1995
NI: 800
TAPP
                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test,
STREET: Four Embarcadero Center,
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
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US-08-473-553A-6
                  NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 139; Conserv
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Sequence 2, Application US/08265628 Patent No. 5821094 GENERAL INFORMATION:

US-08-265-628-2

RESULT 8

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266 EELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQEKVGSGQGEREFQAEVEIISR 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 D---FEGLADAKHINGYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Gaps
                    APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.7%; Score 575; DB 2; Le
39.6%; Pred. No. 1.7e-25;
Live 65; Mismatches 120;
                                                                                                                             McAndrews, Held & Malloy, Ltd. 0 W. Madison St. Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 EGMRPGQSNVTSSYGGSTDYDSSQYNED 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-MAR-1992
ATORNEY/AGENT INFORMATION:
NAME: Pochopien Ph.D., Donald J.
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEPHONE: 312-707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             816 EPTPPGYSLGRSPY -- ENNPSSSRHCDD
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/959,945
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/847,564
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Rothstein, Steven J.
                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held
STREET: 500 W. Madison St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 39.6
Matches 130; Conservative
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                                                                                                                                                    STREET: 500 W. M
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                        19909
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                                                                                                                                                                                                                   COUNTRY:
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US-07-717-331E-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 KIIHRDIKASNILIDFKFEAKVADFGLAKIASD-TNTHVSTRVMGTFGYLAPEYAASGKL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           817 LILHRDVKSNNILLDSDFEAHVADFGLAKFLVDGAASECMSSIADSYGYIAPEYAYTLKV 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 PYGGQQQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPPPPSSSGGSDYSDRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641 FSPSRIVITVIAAITGLILISVAIROMNKKKNORSLAWKLTAFOKLDFKSEDVLEC---L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n 16.6%; Score 572.5; DB 2; Length 985; Similarity 34.6%; Pred. No. 2.7e-25; 88; Conservative 65; Mismatches 135; Indels 61;
                                                                                                          NUMBER OF SECTENCES: 11
CORRESCONDENCE ADDRESS: 20
STRESSES: Flehr, Echbach, Test, Albritton & Herbert STRESS: Four Embarcadero Center, Suite 3400
             APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven B.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Claratal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMNNGYDREEMARMVACAAACVRHSARRRPRNSQIVRAL 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-60886/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                        COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/POCKET NUMBER: A-(TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    985 amino acids
                                                                                                                                                                                                      : California
XY: United States
94111-4187
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LENGTH: 985 amino acid
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                                                                                                                                                                                      San Francisco
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GENERAL INFORMATION:
APPLICANT: Meyero
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Best Local Simi.
Matches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 WRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.6%; Score 572; DB 1; Length 857; 32.3%; Pred. No. 2.5e-25;
Sequence 2, Application US/07717331F
Patent No. 5484905
GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/07/717,331F
                                                                                                                                                   NUMBER OF SEQUENCES: BACOGED AT The NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSEE: Yahwak & Associates STREET: 25 Skytop Drive CITY: Trumbull STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: GEOTGE M. YAHWAK
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELETAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 2:
SRQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                June 19th 199
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SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
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FILING DATE: June 1
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                              Connecticut: USA
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Matches 139; Conserv
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Query Match
Best Local Similarity
Matches 133; Conserv
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                                                                                                     LENGTH: 632
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                                                                                   SEQ ID NO 77
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                                                                                                                                APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhulzen, Niels
TILLE OF INVENTION: Compositions Isolated from Plant Cells
TILLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TILLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TILLE REPREME: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DAIE: 1999-01-12
SOFTWARE: FASTSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Strabbla, Timothy
APPLICANT: Mieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 GSPLOSCNESNNASSASNPIMASSPSMISG----SLPVHRNNSSTQLSKGDIIAIVVGD 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 VALLVIV--TLICLLCKKKRREBEDAYYVPPPPPPPPPRAGGPYGGQQQQWRQQNATPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                              105;
                                                                                                                                                                                                                                                                                                                                                                                            Length 666;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 566.5; DB 4;
Pred. No. 4e-25;
3; Mismatches 166;
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; Patent No. 6359198
; GENERAL INFORMATION:
                                                                                 Seguence 68, Application US/09228986
Patent No. 6359198
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                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Pinus radiata
US-09-228-986-68
793 AEHRFAMSSVV
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 157;
                                                                US-09-228-986-68
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APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF EXCUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 SEPLSRGFIAGVIVVSVVLFWLVIAAAMFLRRTLNRETVEEW---
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Patentin Release #1.0, Version #1.30
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                                                                                                                                                           NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
                                                         JS/09/228,986
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STATE: California
COUNTRY: United States
21P: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: 35/C
CURRENT FILING DATE: 1999-01-12
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US-09-228-986-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 KVADFGLAKIASDTN-THVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGR 472
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APPLICANT: Wang, Guo-Liang
APPLICANT: Scng, Wen-Yuang
APPLICANT: Scng, Wen-Yuang
APPLICANT: Scabo, Varoniques and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                   Length 321;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                        Query Match 15.8%; Score 545; DB 1; L
Best Local Similarity 38.0%; Pred. No. 3.2e-24;
Matches 123; Conservative 57; Mismatches 132;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-Jan-1996
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/08537680A Patent No. 5977434 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                NAME: Goldman Wr., Michael L. TELECOMUNICATION INFORMATION: TELEPHONE: (716,253-1000 TELERAX: (716)-263-1600 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICAMI: Ronald, Pamela C.
               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                321 amino acids
                                                                                                                                                                                                     SS: single
                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-447-185-1
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MEDIUM TYPE: Floppy
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STATE: California
COUNTRY: USA
                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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Patent No. 5648599
GENERAL INFORMATION:
APPLICANT: The DATE OF INVENTION: GROUP B.
TITLE OF INVENTION: GENE CONFERRING DISEASE RESISTANCE
TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRGLENCE GENE IN PLANT PATHOGE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 GQGGFGYVHKGYLPSGKEVAVKQLKVGSGQGERE--FQAEVEIISRVHHRHIVSLVGYCI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 AGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSARGLSYLHEDCNPKIIHRD 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 NKDINLLLYEYMPNGSLGELLHGSKGGHLQWETRHRVAVEAAKGLCYLHHDCSPLILHRD 119
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180 YSFGYVLLELIAGKKKPYGEFGEGVD--IVRWYRNTEEBIIQPSDAAIVVAIVDPRL-TGY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 552; DB 2;
42.5%; Pred. No. 1.1e-24;
tive 53; Mismatches 94
                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
RECISTRATION NUMBER: 83.304
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECHMUNICATION INFORMATION:
TELEPHONE: (415) 781-1889
TELEFAX: (415) 388-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 DREEMARMVACAAACVRHSARRRPRMSQIVRAL 548
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STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/111,078
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/447,185
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
      06-JUN-1995
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                   unknown
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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ZIP: 14603
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rochester
STATE: New York
COUNTEY: U.S.A.
FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                         TYPE: amino a STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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243 DRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 KOLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 EGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAK 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : NAME/KEY: Protein
: LOCATION: 1..54
: OTHER INFORMATION: /note= "Tomato Receptor Kinase 1 (TRK1)"
US-08-587-680A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
15.8%; Score 545; DB 2; Length 544;
Best Local Similarity 40.7%; Pred. No. 5.5e-24;
Matches 125; Conservative 59; Mismatches 111; Indels
                                                                                                                                                                                                  NAME: Bastian, Kevin I.
REGISTRATION NUMBER: 34,774
REFERENCE/OCKET NUMBER: 023070-0589400S
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE:
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-UN-1995
FRICH APPLICATION NUMBER: US 65/004,645
FILING DATE: 29-SEP-1995
FRICH APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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526 REVVQML 532
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Search completed: July 2, 2003, 15:16:13 Job time : 21 secs

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2, 2003, 15:13:41 ; Search time 35 Seconds (without alignments) 2125.726 Million cell updates/sec
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3453
1 MSSAPSPGTGSPPSPSNST.....REMEMGKIKRTGQGYSGPSL 647
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/ Cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           440863 segs, 114992915 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                              July
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112:
14:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 4, Appli Sequence 11, Appli Sequence 11, Appl Sequence 17, Appl Sequence 71, Appl Sequence 71, Appl Sequence 71, Appl Sequence 71, Appl Sequence 91, Appl Sequence 916, Appl Sequence 916, Appl Sequence 916, Appl Sequence 916, Appl Sequence 916, Appl Sequence 916, Appl Sequence 911, Appl Sequence 916, Appl Sequence 91
SUMMARIES	US-10-086-464-5 US-10-086-464-5 US-10-086-464-5 US-10-086-464-5 US-10-086-464-1 US-10-086-464-1 US-10-086-464-1 US-10-086-464-1 US-10-086-464-1 US-10-086-464-1 US-10-086-464-1 US-10-101-4648-1 US-10-101-4648-227 US-10-101-4648-822 US-10-101-4648-812 US-10-101-4648-936 US-10-101-4648-936 US-10-101-4648-936 US-10-101-4648-936 US-10-101-4648-931 US-10-101-4648-931 US-10-101-4648-931 US-10-101-4648-931 US-10-101-4648-931 US-10-101-4648-931
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g Query Match Length DB	74-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-
% Query Match	1000 1000 1000 1000 1000 1000 1000 100
Score	34 53 34 53 34 53 34 53 34 53 34 53 34 53 34 53 54 53 54 54 54 54 54 54 54 54 54 54 54 54 54
Result No.	11111111111111111111111111111111111111

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Gaps

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100.0%; Score 3453; DB 9; Length 647; 100.0%; Pred. No. 9.1e-143; Live 0; Mismatches 0; Indels 0;

Query Match 100. Best Local Similarity 100. Matches 647; Conservative

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Sequence 1117, Ap Sequence 1118, Ap Sequence 1119, Ap Sequence 942, App Sequence 943, App	Sequence 810, App Sequence 510, App Sequence 642, App Sequence 809, App Sequence 2, Appl1 Sequence 945, App Sequence 95, Appl Sequence 95, Appl Sequence 95, Appl	Sequence 26, Appl Sequence 915, Appl Sequence 915, Appl Sequence 807, Appl Sequence 807, Appl Sequence 895, Appl Sequence 695, Appl Sequence 18, Appl Sequence 77, Appl Sequence 923, Appl Sequence 923, Appl Sequence 923, Appl Sequence 923, Appl Sequence 923, Appl Sequence 923, Appl	
9 US-09-754-853A-1117 9 US-09-754-853A-1118 9 US-09-774-853A-1119 9 US-10-101-464A-942 9 US-10-101-464A-943	9 US-10-101-464A-810 9 US-10-101-464A-510 9 US-10-101-464A-642 9 US-10-101-464A-809 9 US-10-149-846-2 9 US-10-208-948-16 9 US-10-208-948-16 9 US-10-208-948-16	10 US-02-027-26 9 US-10-101-464A-915 9 US-10-101-464A-915 9 US-10-101-464A-921 9 US-10-101-464A-807 10 US-09-838-955-8 9 US-10-101-464A-895 9 US-10-101-464A-895 9 US-10-101-464A-97 9 US-10-101-464A-97 10 US-09-838-955-7 10 US-09-838-955-7 10 US-09-838-955-7	
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APPLICANT: GORING, Daphne R. et al. TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES FILE REPERBACE: P 25,762-A USA CURRENT APPLICATION NUMBER: US 10,069,464 CURRENT FILING DATE: 2002-02-28 PRIOR APPLICATION NUMBER: US 10,069,304 PRIOR FILING DATE: 2000-02-19 PRIOR APPLICATION NUMBER: US 10,069,304 PRIOR FILING DATE: 2000-08-18 PRIOR FILING DATE: 1000-08-18 PRIOR FILING DATE: 1090-08-19 PRIOR FILING DATE: 1099-08-19 PRIOR FILING DATE: 1999-10-13 PRIOR FILING DATE: 1999-10-13 NUMBER OF SEQ ID NOS: 27 SOFTWARE: PATENTIN VET: 2.1 SEQ ID NO 2 ILENGRAH: 647 TYPE: PRET CORGANISM: Brassica napus
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PSSPSPPSPSSDGLSTGVVVGIAIGGVALLVIVTLICLLCKKKRRRDEEDAYYVPPPPPP 180
                                                                                                                                                                                         AVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHL 360
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                                                                    181 GPKAGGEYGGQQQQWRQQNATPPSDHVVTSLPPPPPRAPSPPRQPPPPPPPPPRASSGGSD
                                                                                                                  YSDRPVLPPPSPGLVLGFSKSTFTYEELARATMGFSEANLLGQGGFGYVHKGVLPSGKEV
                                                                                                                                   541 MSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKKFRKMALGTQEY
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CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR FILING DATE: 2002-02-19
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-08-19
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100.0%; Pred. No. 1e-142;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
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Les 647; Conservative
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LENGIH: 721
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GPKAGGPYGGQQQQWRQQNATPPSDHVVISLPPPPKAPSPPRQPPPPPPPPFMSSSGGSD
                      GPRAGGPYGGQQQQWRQQNATPPSDHVVTSLPPPPRAPSPPRQPPPPPPPPPPPPRGSSGGSD
                                                                    YSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEV
                                                                                                                                                                                                                                                                                                           YVDDSEVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMVACAAACVRHSARRRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNEELHL
                                                                                                                                                                                                               HGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGL
                                                                                                                                                                                                                                                                                                                                                                                                                              MSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKKFRKMALGTQEY
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CURREAL INTOMASTICAN;
TITLE OF INVENTION: PROLINE RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REPREBRUE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: DC/069,304
PRIOR APPLICATION NUMBER: DC/069,304
PRIOR APPLICATION NUMBER: DC/069,304
PRIOR RILING DATE: 2000-08-19
PRIOR RILING DATE: 1909-08-19
PRIOR PLILING DATE: 1999-10-13
PRIOR PLILING DATE: 1999-10-13
PRIOR PLILING DATE: 1999-10-13
FRIOR FILING DATE: 1999-10-13
SPRIOR FILING DATE: 1999-10-13
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Pred. No. 9.1e-143;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10086464
Publication No. US20020199218A1
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US-10-086-464-4
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Best Local S:
Matches 647;
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                                                         PS-----SPSPPSP--SSDG------LSTGVVVGIAIGGVALLVIVTLICLLCKKKRR
                                                                                      QPPPPPPPPPFMSSSG--GSDYS--DRPVLPPPSPGLVLGFSKSTFTYEELARAINGFSEA
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                                                                                                                                                                                                ----DSFY-----PEPMKGNQYQYYGNNNNNASQNY--PNWHLNSQGQNQQSTGGWGG
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Publication No. US2020199218A1

GENERAL INFORMATION:

APPLICANT: GORING, Dapine R. et al.

TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

TITLE OF INVENTION: PSOLINE-RICH EXPRESSIN-LIKE RECEPTOR KINASES

TITLE OF INVENTION: DAPE: 2002-02-28

CURRENT APPLICATION NUMBER: US/10/086,464

PRIOR APPLICATION NUMBER: US 10/069,304

PRIOR APPLICATION NUMBER: US 10/069,304

PRIOR PLICHE DATE: 2000-08-18

PRIOR PLICATION NUMBER: US 60/149,466

PRIOR FILING DATE: 1999-08-19

PRIOR PLICHG DATE: 1999-08-19

PRIOR APPLICATION NUMBER: US 60/159,122

PRIOR PLICHG DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 27
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51.8%; Pred. No. 3.2e-66;
Live 87; Mismatches 142; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          587 SQTSTNADMKKFRQIALSSQEFPVSDCEGTSSNDSRDMG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           579 DSSQENEDMKKFRKMALGTQEY;--NATGEYSNPTSDYG
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Best Local Similarity 51.8%
Matches 368; Conservative
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US-10-086-464-14
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                                                                                                                YSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEV
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PSSPSPSSPSSDGLSTGVTVGIALGGVALLVIVTLICLLCKKKRRDEEDAYYVPPPPPP
                            541 MSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKKFRKMALGTQEY
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TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REPERSENCE: P 25.762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR PILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: PCT/CA00/00966
PRIOR PILING DATE: 2000-08-18
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
SPRIOR FILING DATE: 1999-10-13
SOFTWARE: PALENTING DATE: PALENTING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10086464 Publication No. US20020199218A1 GENERAL INFORMATION:
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363; Conserv
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Mismatches 156;
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                           2 SSAPSPGTGSPPSPSRSTTT-
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              -----SVPGPPSNPSR---EGGSPRPPSSPSPSPSSDGLST 136
                                                           S---GL-----LLLLAVCICICCNRKKKKSPQVNBMHYYNNNPYGGAPSGNGGYYKG- 228
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    ---PTRN 99
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                                                                                           GVVVGIAIGGVALLVIVTIICLLCKKKRRRDEEDA----YYVPPPPPPGPKA-GGPYGGQ
                                                                                                                                      192 QQQWRQQNATPPSDHVVTSLPPPRAPSPPRQPPPPPPPPPPSSSGGSDYSDRPVLPPPS
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                                                                                                                                                                                                                                                                           372 TRLKIALGSÄKGESYLHEDC-----NPKIIHRDIKASNILIDFKFEAKVADFGL
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Publication No. US20020199218A1

GENERAL INFORMATION:

APPLICANT: GORING, Daphne R. et al.

TITLE OF INVENTION: PROLINE RICH EXTENSIN-LIKE RECEPTOR KINASES

FILE REPERENCE: P. 25, 76.-A USA

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US. 10,069,304

PRIOR APPLICATION NUMBER: PCT/CA00/00966

PRIOR PILING DATE: 2000-08-19

PRIOR PLING DATE: 2000-08-19

PRIOR PLING DATE: 1999-08-19

PRIOR PLING DATE: 1999-10-13

NUMBER OF SEQ ID NOWBER: US 60/159,122

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTING DATE: 1999-10-13
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Pred. No. 2e-54;
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Best Local Similarity
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                                                                                                                                             ---APPPTTPSSPPP
                                                               87 GSPP--APVIPPIRNP---PPSVPGPFSNP---SREGGSPRPPSSP-SPPSP----
                                                                                                                                                                                                                                          148 ESPPLOSPPAPPASDPINSPPASPLDFINPPIQPSGPATSPPANPNAPPSPFTVPPKT
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  Gaps
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TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REFERENCE: P 55,762-A
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR PAPLICATION NUMBER: US 10/069,304
PRIOR FILING DATE: 2002-02-19
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1099-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-10-13
169;
Indels
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35.3%; Pred. No. 1.1e-25;
ive 89; Mismatches 133;
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  CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SEQ ID NO 76
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2-10-101-464A-71
; Sequence 71, Application US/10101464A
; Publication No. US200330046728A1
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Eucalyptus grandis
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Matches 184; Conservative
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Publication No. US20030046728A1
Publication No. US20030046728A1
Publication No. US20030046728A1
PUBLICANT: INFORMATION:
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
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                                                                                                                                                                                                               Score 1399; DB 9; Length 731;
Pred. No. 1e-53;
71; Mismatches 181; Indels 101;
                                                                                                                                  CRGANISM: Arabidopsis thaliana
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ilarity 47.3%;
Conservative 71
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     27
NUMBER CF SEQ ID NOS: 27
SCFTWARE: Patentin Ver.
SEQ ID NO 17
LENGTH: 731
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Matches 317; Conserv
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US-10-101-464A-76
                                                                                                                                          ; CRGANISM: AE
US-10-086-464-17
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US-10-101-464A-927
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Patent No. US2002059562A1

GENERAL INFORMATION:
APPLICANT: COSTA & SILVA, OSWALDO DA
APPLICANT: HINES, WOCHA VAN
APPLICANT: HILEEN, NOCHA VAN
APPLICANT: CHEN, ROUTING
APPLICANT: SARRIA-MILLAN, ROBRIGO
ITILE OF INVENTION: PROTEIN KINASE SIRESS-RELATED PROTEINS AND METHODS OF
ITILE OF INVENTION: USE IN PLANTS
FILE REFERENCE: 16313-0032
CURRENT FILIAG DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILIAG DATE: 2000-04-07
WUMBER: OF SEQUENCE: 128
                                                                                                                                                                                                                                                                                       90 PAPVIPPIRNPPPSVPGPP---SNPSREGGSPRPPSSPSPPSPSSDGLSTGVVVGIAIGG 146
                                                                                                                                                                                                                                                                                                                                                       147 VALLVIVILICLICKKKRRRDEEDAYYVPPPPPPGPKAGGPYGGQQQQWRQQNATPPSDH 206
                                                                                                                                                                                                                                                                                                                                                                                                                   207 VVTSLPPPRAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYE 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------FFDVPA--EEDPEVHLGQLK-RFSLR 297
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                                                                                                                                                                                                                                                                                                             252 AALLF-----WRRRK---POEH
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                                                                                                                                                                                                                                                            68; Mismatches 125;
PRICR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR PRILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 969
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 37.28
Matches 175; Conservative
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LENGTH: 749
TYPE: PRT
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RESCUT 11

US-10-101-464A-927

Squence 927, Application US/1010164A

Publication No. US20030046728A1

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Highins, Collean M.

ITILE OF INVENTION: Compositions Isolated from Plant Cells

ITILE OF INVENTION: and Their USe in the Modification of Plant Cells

ITILE OF INVENTION: and Their USe in the Modification of Plant Cells

ITILE OF INVENTION: and Their USe in the Modification of Plant Cells

ITILE OF INVENTION: and Their USE in the Modification of Plant Cells

ITILE OF INVENTION: and Their USE in the Modification of Plant Cells

ITILE OF INVENTION: and Their USE in the Modification of Plant Cells

FIGHS APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 1999-01-12

PRIOR PILING DATE: 1999-01-12

PRIOR PLING DATE: 1999-11-01

PRIOR PLING DATE: 1999-11-01

PRIOR PLING DATE: 1999-11-01

PRIOR PLING DATE: 1999-11-01

PRIOR FILING DATE: 2000-01-11

WUMBER OF SED ID NOS: 989

SOFTWARE: FastSED for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 GLVLGFSKST-----FTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGKE 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 --LHLHGEGRETMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475 VDANNVYVDDSLYDWARPLLNRASEQGDFEGLA---DAKMNNGYDREEMARMVACAAACV 531
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                                                                                                                                                  Gaps
                                                                                                                                            84;
                                                                                       Length 749;
                                                                                                                                               Indels
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                                                                                                                                            160;
                                                                                                                                                                                                                                                                                                            159 LCKKKRRR---DEEDAYYVPPP---PPPGPKAGGP---
                                                                                       20.9%; Score 722; DB 10; 35.6%; Pred. No. 2.3e-24;
                                                                                                                                            76; Mismatches
) ORGANISM: Physcomitrella patens
US-09-828-313-27
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QPEPEFRPPMSEVVQAL 719
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                                                                                                                                            Matches 177; Conservative
                                                                                                              Local Similarity
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                                                                                       Query Match
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RESULT 13
US-10-101-464A-74
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Publication No. US20030046728A1

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

TITLE OF INVENTION: Compositions Isolated from Plant Cells

FILE REFERENCE: 11000,1020c2

CURRENT APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2002-03-18

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-01-10

PRIOR FILING DATE: 1999-01-10

PRIOR FILING DATE: 1999-01-10

PRIOR FILING DATE: 1000-01-11

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 1000-01-11
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                                                      263 FIYEELARAINGESEANLLGQGGFGYVHKGVLPSGKEVAVKQLK----VGSGQGEREFQA 318
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                                                                                                                                                                                                                                    ---GLAERWEASQRVESNKG-----KPHEFSSSDRYSDLTDDSS
                                                                       319 EVELISRVHHRHLVSLVGYCLAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIAL
                                                                                                                           439 FGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVD----ANNVYVDDSLVDWARPLL
                                                                                                                                                                                                                                                                                           495 NRASEQGDFEGLADAKMNNGYDREEMARWYACAAACVRHSARRPRMSQIVRALEGNVSL
                              Gaps
                            47;
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    Length
                              Indels
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Pred. No. 1.4e-23;
1; Mismatches 179;
                            92;
  DB 9;
Score 704.5; DB 9
Pred. No. 1.1e-23;
                            71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 989
SOFFWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 80
SEQ ID 707
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34.0%;
 20.4%;
41.8%;
                            Matches 151; Conservative
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Best Local Similarity 34.0
Matches 178; Conservative
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US-10-101-464A-80
               Similarity
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 Query Match
Best Local
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APPLICANT: Micuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
APPLICANT: Higgins, Colleen M.
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPERENCE: 11060-1030c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/728,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 06/152,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 07/152,866
PRIOR FILING DATE: 1999-11-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       620 QSLWEWATPQLH------DIDALAKWVDPALKGSYPAKSLSRFADIIALCIQPEPEFRPP 673
      ---GSDYSDRPVL 247
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                                                                            :: | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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195 WRQQNATP--PSDHVVTSLPPPRAPSPPRQPPPPPPPFMSSSG--
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68; Mismatches
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NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
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Publication No. US200300465728A1
SERMERAL INFORMATION:
APPLICANT: Strabala, Timothy
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Matches 147; Conservative
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ch completed: July 2, 2003, 15:20:53 time : 37 secs
                 RESULT 15
US-10-219-220-263
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APPLICANT: Nieuwenthuizer, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/128,986
PRIOR PELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR PELING DATE: 1999-01-10
PRIOR APPLICATION NUMBER: PCT/US00/00724
PTRKRIALGAARGLLYLHEQCDPKIIHRDVKAANILLDEYFEAVVGDFGLAKLLDHRDSH 473
                                                                                                                 VSTRVMGTFGYLAPETAASGKLTEKSDVFSFGYTLELITGRRPVD----ANNVYVDDSL 486
                                                                                                                                                                 VDWARPLINRASEQGDFEGLADAKMNNGYDREEMARNYACAAACVRHSARRPRASQIVR 546
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:::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| :::|| | :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| ::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 ALEGNVSLSDLNECMRPGQSNVYS-----SYGGSTDYDSS 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||: |:: | :: | : | 11|
587 MLBGD-GLTERWEILQKIETPRYRVTEIPITYSELVEEDSS 626
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Publication No. US20030046728A1
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GENERAL INFORMATION
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US-10-101-464A-812
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APPLICANT: Flinh, Barry
APPLICANT: Flinh, Barry
APPLICANT: Lasham, Aunette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
CURRENCE: 11000.1022a1
CURRENCE: 11000.1022a1
CURRENCE: 1000.1022a
CURRENCE: 1000.1022a1
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR APLICATION NUMBER: 0.S. No. US20030082724A1 09/325,932
PRIOR PLILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 263
LENGTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 FMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHK 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 NVLLFDDFKAKIADFNLSNQAPDMAARLHSTRVLGTFGYHAPEYAMTGQLTQKSDVYSFG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 GVLPSGKEVAVKQLKVGS-GQGEREFGAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 VPNNNLELHLHG------EGRPINEWSTRLKIALGSAKGLSYLHEDCNPKITHRDIKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 NILIDFKFEAKVADFGLAKIASDINTHY-STRVMGTFGYLAPBYAASGKLTEKSDVFSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 VVLLELITGRRPYDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 YKMSEGAKSGPPOKIAPIEAPALSL-----EELKEATDNFGAKALIGEGSYGRVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%; Score 661; DB 9; L. 43.1%; Pred. No. 5.2e-22;
Live 57; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 MVACAAACVRHSARRRPRMSQIVRALE 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 263, Application US/10219220
Publication No. US2003008724A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 43.18
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pinus radiata
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 15:20:18; Search time 53 Seconds (without alignments) 1173.565 Million cell updates/sec July Run on:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST.....REMENGKIKRTGQGYSGPSL 647 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000500000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. Wo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable protein k	hypothetical prote		hypothetical prote		^	cal		ب	protein F20B24.6 [	hypothetical prote		probable serine/th				serine		protein kinase hom	probable protein k	hypothetical prote	probable protein k	probable receptor	hypothetical profe		hypothetical profe			. ψ
SUMMARIES	Ω	F84564	A96529	T05264	D96728	D96711	F86387	B86369	T04455	A96563	GB6239	C96728	T01477	T01502	E84587	696593	T01086	T01711	A86146	T05994	B96609	E96602	D84860	G96602	G86227	G84510	н96740	T47793	F96602	D86466
	EQ.	71					7														7	0				ä	ď	C)	7	
	Length	633	669	674	710	708	760	731	731	509	715	394	321	707	435	676	492	450	497	523	495	858	494	2062	482	520	109	512	1029	628
ф	Query Match	50.6	50.1	48.9	43.9	42.3	41.5	41.0	40.5	٠	35.7	29.6	28.2	23.6	23.2	22.4	22.4	22.3	22.1	21.9		21.6	-	21.5	21.2	21.0	21.0	20.9		20.8
	Score	1748.5	1729	1687	1515.5	1459.5		1415.5	1399	1397	1233	1022	973	816.5	802	774	~	769.5	764	757	749.5	45	744.5	743.5	732.5	726.5	724.5	722.5	719	717
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۰,	712.5		386	7	T49152	serine/threonine-s
_	711		553	C)	T14354	probable somatic e
Δi	703		381	N	C96791	hypothetical prote
<u></u>	700		426	C4	T00848	probable serine/th
	699.5	20.3	395	C4	T48301	protein kinase-lik
10	597	20.2	942	N	C96574	hypothetical prote
10	695	20.1	481	C)	TC5270	probable serine/th
37	692	20.0	605	N	T50817	protein serine/thr
œ	690.5	20.0	979	N	D96574	hypothetical prote
•	689	20.0	588	(A	E96633	probable Serine/Th
_	989	19.9	750	N	D86245	hypothetical prote
41	585.5	19.9	423	Ŋ	B86214	hypothetical prote
~1	685	19.8	854	N	A96574	protein F12M16.30
~	683	19.8	424	~	G84686	probable protein k
	582.5	19.8	607	N	G84630	probable LRE recep
	682	19.8	426	7	T52285	serine/threonine-s

## ALIGNMENTS

339 IAGAKRLLYYEFVPNNNLELHLHGEGRPIMEWSTRLKIALGSAKGLSYLHEDCNPKIIHR 398

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da ço	348 IADGQRMLVYEFVPNYTLEYHLHGKNLPVWEFSTRLRIALGAAKGLAYLHEDCHPRIIHR 407 399 DIKASNILIDEKEEAXVADFGLAKIASDINTHVSTRVMGTFGYLAPBYAASGKLIFEKSDV 458	QY 299 EVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCI-AGAKRLLVYEFVPNNNLE 357  -
Q. qa	t ny ny	QY 358 LHLHGEGRPTMEMSTRLKIALGSARGLSYLHEDCNPKIIHRDIKASNILLIDEKFEAKVAD 417 
δ. Q		QY 418 FGLAKIASDINTHVSTRVMGTFGYLAPEYAASGKLIFEKSDVFSFGVVLLELITGRRPVDA 477
O.y		QY 478 NNVYVDDSLYDWARPLIARASEQGDFEGLADAKMNNGYDREEMARWVACAAACVRHSARR 537 : ::              ::   :   :   :
RESULT :		QY 538 RPRMSQ:VRALEGUNSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKKFRKMALGT 597
hypothe C;Specie C;Date: C:Access	hypothetical protein F13F21.28 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002 C;Accession: A66529	QY 598 QEYNATGEYSNPISDYGLYPSGSSEGQTIREMEMGKIKRIGQG 641 ::    :
R; Theold Chin, ( ansen, h	ogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C.; Alonso, W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.E.; Dewar, K.; Hughes, B.; Euizar, L.	RESULT 3
A; Author C.A.; Li Rizzo, h	tus, Bib-820, 2000 T. Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. I. J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, 4.; Rooney, T.; Rowley, D.; Sakano, H.	probable serine/threonine-specific protein kinase (EC 2.7.1) T4L20.20 - Arabidopsis C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 17-Mar-2000
A; Authon ker, M., A; Title: A; Refere	A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, L.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A:Title: Sequence and analysis of chromosome l of the plant Arabidopsis. A:Reference number: A86141; MUID:21016719; PMID:11130712	C.Accesion: T02264 R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; ewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, September 1998
A; Acces: A; Status A; Molecu	A; Accession: A56529 A; Status: preliminary A; Status: preliminary A; A	A, Acteriance number: £13400 A;Accession: T05264 A;Mesiques: 1-674 <brv></brv>
A; Keslaues: A; Cross-refe C; Genetics:	A; Resudues: 1-099 <s.10> A; Acss-references: GB:AE005173; NID:95430769; FIDN:AAD43169.1; GSPDB:GN00141 C; Genetics:</s.10>	A,Cross-references: EMBL:AL023094 A;Experimental source: cultivar Columbia; BAC clone T4L20 C:Generics:
A,Gene: A,Map pc C,Superí	A;dene: F13F21.28 A;Map position: 1 C;Superfamily: unassigned Ser/Ihr or Tyr-specific protein kinases; protein kinase homolq	A.Map position: 4 A.Introns: 180/1; 221/1; 381/1; 421/1; 444/3; 470/2; 518/3; 583/3 A.Note: T4L20.20
Query Match Best Local S Matches 372	į	C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: phosphotransferase; protein kinase
ΟŸ	2 SSAPSPGTGSPPSPSNSTTTTPPPAASAPPPTTPSSPPPSTIPTSPPP 50	Query Match  Query Match  Best Local Similarity 51.8%; Pred. No. 3.3e-47;  Matches 368; Conservative 87; Mismatches 142; Indels 114; Gaps 25;
DB QY	9 NSFPAPPPSPPSPPSSNDQQTTSPFPSDNQETTSPPPPSSPDIAPPPQQQQESPPPPP 68 51SSRSTPSAPPSPPTPSTPGSPPPLPQPSPPAPT	QY 1 MSSAPSPGIGSPPSDFSNSTTTPPPASAPPTTPSSPPPPSTIPTSPPSSRSTFPSAPP 60 :  : :      :
oy oy	69 ENSSDGSSSSPPPPSDSSQQSPPP-PSTSPPQQSDNNGNKGNNNENNKGNDGSSGDG 127 87 GSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPSSSPSPSPSSDGLSTGVVVGIAIGG 146	QY         61 PSPPTPSTPGSPPPLPQPSPPAPTTPGSPPA-PVTPPTRN 99            :      :     :
DP Cy	- PPPS	13
qq		137
ඊ සි	204 SDHVVTSLPPPPKAPSPPRQPPPPPPPPPFMSSSGGSDY 241 :  : :      : :       : :	Db 179 SGLELLLAVCICICCNRKKKKSPQVNHMHYYNNNPYGGAPGONGGYKG- 228 Ov 192 Onomponentimest database and proper a proper
Qy Db	., .,	229TPQDHVV-NMAGQGGGNWGPQQPVSGPHSDASNLTGRIALFSPQ 252 PGIVIGERKSHEWEFIABARWSEGANII GOGGERVUURKUU DGGREWAVENI KONGOO
A.		zoz folylogielieblikkingfoernilogigefgiyhafursurevaykunygogi

::     :	QY 163 KRRRDEEDAYYVPPPPPPGFKAGGFYGGQQQWRQQNATPPSDH 206
QY 312 GEREPQAEVELISRVHHRELVSLVGYCIAGAKRLLVYEEVPNNNLELHLHGEGRPTMEWS 371	Db 260 KRNIDAYSDSTEPPSNFSIKSDGFLYGQNPTKGYSGPGGYNSQQQS-NSGNS 312 Qy 207 VVISLPPPPRARSSPPRQPPPPPPPPPRASSGGSDYSDRPVLGPPSPGIVLGFSKSTFTYE 266
QY 372 TRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKPEAKVADFGL 420	313
4 /	
481	OY 327 HHRALVSIVGYCIAGAKRLLVYEFVPNNNLELHLEGEGRPIMEMSTRLKIALGSAKGLSI 385
Db 510 EMEDSLYDWARPLCLKAAQDGDYNQLADPRLELNYSHQEMYQMASCAAAAIRHSARRRPK 569 QY 541 MSQIVRALEGNYSLSDLNBOMRPGQSNYYSSYGGSTDYDSSQYNEDMKK 589	Qy 387 LHEDCNPKIIHRDIXASNILIDFKEFAKVADFGLAKIASDINTHVSTRVMGTFGYLAPEY 446
570 MSQVQKLIPLVGSIIVRALEGDMSMDDLSEGTRFGQSTYLSPGSVSSETDAG	OY 447 AASGKLIEKSDVFSFGVVLLELIIGRRPVDANNVYVDDSLVDAARPLLNRASEQGDFEGL 506
QY   590 FRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGGTTREMEMGKIKRTGQ 640	Db 525 AQSGKLIDRSDVFSFGVVLLBLITGRKPVDQYQPLGEBSLVEWARPLLHKALFTGDFSEL 584 OV 507 ADAKMMAYDPEPHADKTARAAAYTGDGADDDWGGTTVBLEGANGGTGTTVBPGMDGGGG 566
;	585 VDRRIEKHYVENEVERMIETAAACVRHSGERRPRWYQVVRALDSEGDMGDISNGNKVGGS
D96728 hypothetical protein F24J13.3 [imported] - Arabidopsis thalians C:Species: Arabidossis thaliana (monse-ear cress)	SYGGSTDYDSSQYNEDMKKERKALGTQEYNATGEYSNPTSDYGLYPSGSSEGQT
C:Date: 02-Mar-2001 *Sequence_revision 02-Mar-2001 *text_change 31-Mar-2001 C;Accession: D96728	
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.	S 693 GU
Nature 408, 816-823, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C	RESULT 5
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.H.; Sun, H.; Tallon, Rer, M.; Wu. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Dayls, R.W. A; Filtle: Sequence and analysis of chromosome 1 of the plant brahidomsis	
A; Reference number: A86141; MOID:21016719; PMID:11130712 A. Accession: D96728 A. Accession: D96728	C.J.: Federspiel, D90. A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo: C.Jin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
A.Status: preliminary A.Molecule type: DNA A.Pasidnes: 1-710, como.	ansen, N.F.; Hughes, B.; Hutzar, L. Nature 408, 816-820, 2000
A.Cross.references: GB:AE005173; NID:g6175155; PIDN:AAF04882.1; GSPDB:GN00141 C;Genetics:	A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzīt Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
J13.3 ion: 1	A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallcker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, RW. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidosis.
Query Match	A; Reference number: A86141; MUID:21016719; PMID:11130712 A; Accession: D96711 A; Status: preliminary
OY 2 SSAPSP-GTGSPPSPSNSTTTTPPPASAPPPTTPSSPPPSTI 44	A;Molecule type: DNA A;Residues: 1-708 <sto> A;Residues: 1-708 <sto> C;Acrost-references: GB:AE005173; NID:g5734709; PIDN:AAD49974.1; GSPDB:GN0C141</sto></sto>
45 PISPPSSRSTPSAPPSTPGEP   1111	A;Gene: F24J5.8 A;Map position: 1
PPFFDAPFTIVFPPTIDSPPPESTNSPP	Query Match 42.3%; Score 1459.5; DB 2; Length 708; Best Local Similarity 41.8%; Pred. No. 5.5e-40; Matches 317; Conservative 90; Mismatches 127; Indels 225; Gaps 21;
Db 142 PPEQLPPPASSPQGGFKKPKKHHPGPATSPPAPSAPATSPPAPPAPPRAPPRASSHALPPKST 201	QY I MSSAPSPGTGSPPSNSTT-TTPPPASAP-PPTTPSSPPPSTIPTS 48
105 FGPPSNPSREGGSPRPPSSPSPGLSTGVVVGIALGGVALLVIVTLICLICKK 1	MATTPVQPPVSNSPPVTSPPPNNATSPATPPPVTSPLPPSAPPPNNAPPPSFPVTTSP
DD 202 AAGGPLTSPSRGVPSSGNSVPPPANSGGGYQGKTMAGFAIAGFAVIALMAVVFLVRRK 259	1 QY 49 PPSSRSTPSAPPPSPPTPSTPGSPPPLPQPSPPAPTTP 86

Query Match	SDSKRPVHPSPPSPPETLPPPKESPDPLPSNSSSPPTLL PPSSPSPPSPPTLL	QY 280 LLGQGGGGYVHKGYLPSGKEVAVKQLKVGSGGGEREFQAEVEIISRVHHRHLVSLVGYCI 339  [	QY 460 SPCVVLLELITGRREVDANNYYDDSLVDWARPLLNRASEGGDFEGLADARMNNGYDREE 519	RESULT 7 B86369 hypothetical protein F508.10 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear crees) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: B86369 C;Accession: B86369 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor Chin, C.W.: Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, B16-820, 200 A;Authors: Burner, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzie Rizzo, M.; Rooney, T.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc ker, M.; Ru, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Scatus: preliminary A;Molecule type: DNA
	QY         235        SSGGSDYSDRPVILPPP		Db 604 FILL	., O.; Alonso,; Dewar, K.; K.; K.; Kim, C. R.; Marziali, H.; Fallon, 141

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protein kinase ho

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318 432 378 4.92 4.35 50 555

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probable protein kinase 60711-62822 [imported] - Arabidopsis thaliana CSPecies: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: A96563
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Aloi Chin, C.K.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
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                                                                                                                                                                                                           40.5%; Score 1399; DB 2; Length 731;
47.3%; Pred. No. 4.5e-38;
Live 71; Mismatches 181; Indels 101;
                                                                                             A,Map position: 4
A;Introns: 326/1; 476/1; 505/1; 528/3; 557/2; 606/3; 660/3
A;Note: F4D11.90
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 GGVIVGALLILIEGILETETRATRNRNNSSSAHHOSKTP----
                              A;Cross-references: EMBL:AL022537
A;Experimental source: cultivar Columbia; BAC clone F4D11
C;Genetics:
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321; Conservative
A; Residues: 1-731 <STO>
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protein F24J13.2 [imported] - Arabidopsis thaliana
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, T.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Status: preliminary
A; Mclecule type: DNA
A; Residues: 1-509 <STO.
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hużzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                     79 SPPAPTIPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSSPSSDGLSTGV 138
                                                                                                                                                 GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                             VVGIAIGGV-ALLVIVTLICLLCKKKR---RRDEEDAYYVPPPPPPPPPRAGGPYGGQQQQ 194
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                                                                                                                                                                                                                                                                                               SPPAPEFPSTTPDTATSPAPS-QPSIIGPSSL----APFPETTINIDGGSRNVALTGL
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        255 VLGESKSTFTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGER
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                                                                                                                                           A;Cross-references: GB:AE005173; NID:g10645450; PIDN:AAG21566.1; C;Genetics:
A;Gene: F13K6.9
                                                                                                                                                                                                                    Length 509;
                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                   7; DB 2;
4e-38;
                                                                                                                                                                                                                                               120;
                                                                                                                                                                                                                                             70; Mismatches
                                                                                                                                                                                                                   Score 1397;
Fred. No. 4e
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                                                                                                                                                                                                              Query Match 40.5
Best Local Similarity 52.5
Matches 296; Conservative
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H.; Tall
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                                                                                                                                                                 PIDN: AAF17672.1; GSPDB:GN00141
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    Southwick, A.M.; Sur,
                                                                                                                                                                                                                                                                                                                                                                     SSAPSPGTGSPPSPPSNSTTTTPPPASA -- PPPTTPSSPPPPSTIPTSPPPSSRSTPSAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 AGVFFVRRKQKKGSSSPRSNQYLPPANVSVNTEGFIHXRQKPGNGNSS---AQNSSPDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 EELARATNGFSEANLLGQGGFCYVHKGYLPSGKEVAVKQLKYGSGQGEREFQAEVEIISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 HVVISLPPPPKAPSPPRQPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTY
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A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MJID:21016719; PMID:11130712 A; Accession: G86239 A; Status: preliminary
                                                                                                                                                                                                                                                                                                            198;
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                                                                                                                                                                                                                                                                                                          Mismatches 163;
                                                                                                                                                                                                                                                                 Score 1233; DB 2;
Pred. No. 8.1e-33;
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                                                                                                                   A;Molecule type: DNA
A;Residues: 1-715 <STO>
A;Cross-references: GB:AE005172; NID:96573752;
C;Genetics:
A;Gene: F20B24.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGSPPAPVTPPTR-----NPP-
                                                                                                                                                                                                                                                                                                          84;
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473

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probable serine/threonine-specific protein kinase (EC 2.7.1.-) T10M13.2 - Arabidopsic C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 19-Peb-1999 #sequence_revision 19-Feb-1999 #text_change 04-Mar-2000
C; Accession: T01502
R; Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; (Marthenssen, R.; McComble, W.
Marthenssen, R.; McComble, W.
Submitted to the EMBL Data Library, May 1997
A; Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A; Reference number: 214346
A; Reference number: 214346
A; Accession: T01502
A; Accession: T01502
A; McCession: T0
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A. CLOSS-references: EMBL. AF001308; NID: 92104523; PID: 93912917
A. Experimental source: cultivar Columbia
C. Genetics:
A. Map position: 4S
A. Introns: 132/1; 256/1; 327/1; 451/1; 532/2; 581/3
A. Note: T10M13.2
C. Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C. Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 SDRPVLPPPSPGL---VLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFSKPSMKRNAQSPGAGLADIAPAQSSNGVLPDALTQPPLSPSISNCCKSDMVLKRRSIG 146
                                                                                                                                                                                                                                                                       homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 EVAVKOLKVGSGOGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIHGEGRPTMEWSTRLKIALGSAKGLSYLHEDC----NPKIJHRDIKASNILIDFKFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 KVADFGLAKIASDTNTHVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 PVDANNVYVDDSLVDWARPLLINRASEQGDFEGLADAKMNGYDREEMARMVACAAACVRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                               A;Map position: 1
A;Introns: 136/1; 166/1; 189/3; 215/2; 264/3
C;Superfamily: kinase-related transforming protein; protein kinase
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                                                                                                                                                                                                                                                                                                                                                28.2%; Score 973; DB 2; I
61.7%; Pred. No. 7.1e-25;
iive 45; Mismatches 62;
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                                        A; Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- APGPPS----
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 61.7%
Matches 192; Conservative
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                                                                             C;Genetics:
A;Gene: ATSP:F1707.1
                                                                                                                                                                                                                                                                                                                                                Query Match
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: 026728
R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Coway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudnes, B.; Huides, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein kinase homolog F1707.1 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Spate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Nov-1999 (S.Accession: T01477 (S.A. Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, rz. Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N. Submitted to the EMBL Data Library, June 1998 (A.) Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.

A.Reference number: 214334 (A.) Accession: T01477 (A.) A.Status: translated from GB/EMBL/DDBJ (A.) A.Status: translated from GB/EMBL/DDBJ (A.) A.Status: Lanslated from GB/EMBL/DDBJ (A.) A. A.Status: Lanslated from GB/EMBL/DDBJ (A.) A.Status: Lanslated from GB/EMBL/DDBJ (A.) A.Status: Lanslated from GB/EMBL/DDBJ (A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 SGPRRPRMYQYLRALDSRGDMGDICNGIKVGQS-----STCDDSGQNHSYIKDVGSI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE005173; NID: 96175154; PIDN: AAF04881.1; GSPDB: GN00141 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Gene: F24J13.2
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 SDRPVLPPPSPGL---VLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLEGEGRPTMEWSTRLKIALGSAKGLSYLHEDC----NPKIIHRDIKASNILIDFKFEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1022; DB 2;
Pred. No. 2.4e-26;
54; Mismatches 82,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.65
Best Local Similarity 57.05
Matches 207; Conservative
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109

DD 147 CHCVYPIKLDILLLNVSETPSWNMFLNEFATQLGELPHQIELINFYVLSLSRMNISMDIT 206	Oy 294 LPSGKEVAVKQLKVGSGQGEREFQAEVELISRVHHRHLVSLVGFCIAGAKELLVYEFVPM 353
110	DD 59 MEDGTEVAVKLITEDNQNRDREFIAEVEMI.SRLHHRNLVKLIGICIEGRTRCLIYELVHN 11
207 PHSGISFSASQASAINSSLI	QY 354
CY 130 SSDGLEIGVVVGIAIGGVALLVIVEGCILCKKKRRDEEDAYYP 175 	DD 119 GSVESHIH-EG-TLDWDARLKIALGAARGLAYLHEDSNPYVIHRDFRASNVLLEDDFTP 17
PPPFMSS	DD 176 KVSDPGLAREATEGSQHISTRVMGTFGYVAREXAMTGHLLVKSDVESTGVVLLELLIGRR 473
318	QY 474 PVDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMVACAAACVRH 53
OY 236 SGGSDYSDPPPPSPGLVLGFSKSIFTYEELARAINGFSEANLLGQGGFGTVHKGVLP 295	Db 236 PVDMSQPSGEBNLVTWARPLLANREG-LEQLVDPALAGTYNFDDMAKVAALASMCVHQ
	7 d
354 NNLELHLHGEGRPTMEWSTREKTAHRNIVKLYGYYSSRDSSQHLLCYELYPN 354 NNLELHLHGEGRPTMEWSTREKTALGSAKGLSYLHEDCNPKITHRDIKASNILLD 1	QY 585 EDWKKFRKMALGTQEYNATGEYSNPTSDYGLYPSGSSS 622  1 : : :   :   :
QY 409 FKFEAKVADFGLAKIASD-TNTHVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLE 457	
468 LITGRREVDANNYYVDDSLVDWARPLLNRASBQGDFEGLADAKMNGYDREEWARMYACA : :         :::   :	
QY 569 YSSYGGSTDYDSQQNDDMKKER 591   1	Rizzo, M.; Rochey, T.; Rowley, D.; Sakano, B. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallıker, M.; Wi, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
RESULT 14	A:Reference number: A86141; MOID:21016719; PMID:11130712 A:Accession: 965593 A:Status: preliminary
le protein kinase [imported] - Arabidopsis thaliana ies: Arabidopsis thallana (mouse-ear cress) : 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change 17-May-2002 Ssion: B84587 X.; Kaulf_S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fu	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-676 <sto> A; Cross references: GB: AE005173; NID: g10645416; PIDN: AAG21533.1; GSPDB: GN00141 C; Genetics: A; Genetics: A; Man position: 1</sto>
i.,	Venter, J
A; Accession: E84587 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-435 <sto></sto>	QY 248 PPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGGGGFGYVHKGVEPSGK 298
A;Cross-references: GB:AE002093; NID:94512705; PIDN:AAD21758.1; GSPDB:GN00139-C; Genetics: A;Gene: At291300 A;Map position: 2	QY 299 BVAVKQLKVGSGQGERBFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPANNILEL 358
C;Superfamily: kinase-related transforming protein; protein kinase homology Query Match 23.2%; Score 812; DB 2; Length 435; Best Local Similarity 45.7%; Pred No. 2, 26-10.	OY 359 HLHGBGRPIMEMSTRLKIALGSAKGLSYLHEDCNPK-IIHRDIKASNILJDFKFEAKVAD 417
Matches 182; Conservative 68; Mismatches 122; Indels 26; Gaps 9;	QY 418
QY 234 SSSGGSJYSDRPVLPPPSPGLVLGFSKSTFTYEBLARATNGFSEANLLGGGGFGYVHKGV 293	Db 523 FGLARWQPDGELGVDTRVIGTFGYLAPBYAQSGQITERADVKSFGVVLELITGRKAMDI 582  Oy 478 NNVVVDDSIVDWARPIINRAGROCDFFGIADAKMNNGVDRSWAPMVACABAANYDBGABD 537
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583 YRPKGQQCLIEWARSLL---EEYAVEELVDPRLEKRYSETQVICMIHTASLCIRRDPHL 638

538 RPRMSQIVRALEGNVSLSDLN 558 |/||||::||||::::::: 639 RPRMSQVLRLLEGEMIMNEIS 659

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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

RAPBL, ANO28099; AAKJ1955.1, ...

RICEPPO: IPR000290; Ser_thr_EMinase.

RICEPPO: IPR001295; Prich_extensn.

RICEPPO: PR001295; TYL_PKinase.

RICEPPO: PR001295; TYL_PKinase.

RICEPPO: RENO1295; PR01217; PRCHEXTENSN.

REINTS; PR01017; PRCHEXTENSN.

RENOTE: PR00109; TYRKINASE.

RODOM; PR00109; TYRK: 1.

RART; SM00219; TYRK: 1.

RART; SM00219; TYRK: 1.

ROSITE: PS00107; PROTEIN KINASE_LOW; 1.

RROSITE: PS00101; PROTEIN KINASE_LOW; 1.

RROSITE: PS00108; Rinase; Serine-Protein kinase; Transferase.

SEQUENCE 647 AA; 68482 MW; A69ABAOCOD5CA203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor protein kinase PERKI.
Brassica napus (Rape).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TAXID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Silva N.F., Goring D.R.;
"Characterization of a novel Brassica napus receptor protein kinase
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0919c5
0943i7
0943i7
096438
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09fu38
08rww0
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Q9sk72
Q9lic9
Q8w0n1
Q94kd9
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01-JUN-2001 (TIEMBirel. 17, Last sequence update)
01-MAR-2002 (TIEMBirel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3453; DB 10;
Pred. No. 6.4e-216;
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                09ASK4
09AY15
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Best Local Similarity
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Q9cal8 arabidopsis
091v50 arabidopsis
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09c660 arabidopsis
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1514.915 Million cell updates/sec
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Capyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2002 (TrEMBLrel. 21, Last annotation update)
Protein kinase-like protein (ATS924550/M0B24_8) (Hypothetical 69.3 kDa
                                     1 MSSAPSPGTGSPPSPSPSNSTTTTPPPASAPPPTTPSSPPPPSTTPTSPPPSSRSTPSAPP
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       Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko I., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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   Mismatches
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MEDLINE=20363099; PubMed=10907853;
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01-0CT-2000 (TrEMBLRel. 15,
01-JUN-2002 (TrEMBLRel. 21,
647; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki T.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Torlumi M., Yamada K.,
Tamania Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                   SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Rarlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishidad J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Tamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 DAYYVPPPPPPPRAGGPYGGQQQQMRQQNATPPSD-HVVTSLPPPPRAPSPPRQPPPPP
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features of the regions of 4,251,695 bp covered by ninety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Sukurai T., Theologis A., Davis R.W.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARLYR: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
--- BMBL, AB0220746; BAB02007.1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Hypothetical protein; ATP-binding; Kinase;
Serine/threopine-protein kinase; Transferase.
SEQUENCE 652 AA; 69271 MW; 35005EE29FE8602F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
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87.0%; Pred. No. 2.1e-182;
ive 24; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002965; P. rich_extensn.
InterPro; IPR00290; Ser_thr_pkinase.
InterPro; IPR004040; STr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO0109; TYRKINASE.
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EMBL: AY093065; AAM13064.1;
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Matches 574; Conservative
                               3AC clones.";
7:217-221(2000)
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                                  and BAC
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                                                           DNA Res.
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               PPSLPPPSPPGSLT---PPIPQPSPSAPITP-SPPSFTTPSNPRSPPSPNQGPPNTPS--
                                                                  TPSAPPPSPPTPSTPGSPPPLPQPSPPAPTTPGSPPAPYTPPT-RNPPPSVPGPPSNPSR
                                                     BGGSPRPPSS--PSPPSPSSDGLSTGVVVGIAIGGVALLVIVTLICLLCKKKRRR--DEE
                                                                                                       DAYYVPPPPPPPPRAGGPYGGQQQWRQQNATPPSD-HVVTSLPPPPKAPSPPRQPPPPP
                                                                                                                       PPP-FMSSSGGSDYSDRPV1PPPSPG1VLGFSKSTFTYEELARATNGFSEANL13QGGFG
                                                                                                                                                                                                               YVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLV
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                                                                                                                                                                                                                                                                                   LITGRRPVDANNVYVDDSLVDWARPELNRASEQGDFEGLADAKMNNGYDREEMARWYACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKFRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMGKIKRTGQGYSGPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative receptor protein kinase PERK1.
00452F10.5.
0ryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae, Oryza.
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EMBL; AP003434; BAB78668.1; -.
InterPro; IPR00019; EUK_pkinase.
InterPro; IPR000847; HTH_LIYSN.
InterPro; IPR00290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00065; pkinase; 1.
SMART; SM00201; EUK_pkinase; 1.
SMART; SM00210; STKC; 1.
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PROSITE; PSOG107; PROTEIN_KINASE_ATP; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597
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Sasaki T., Matsumoto I., Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SULCHMICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk K., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (APR-2001) to the BNBL/GenBank/DDBJ databases.
ENSE: AF370509; AAK43886.1; -.
ERUSI: AF370509; AAK43886.1; -.
ERUSI: SEPPO: IPRO00719; EUk pkinase.
InterPro: IPRO02290; Ser_thr_pkinase.
                                       YVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGTCIAGAKRLLV
                                                                                           LITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNGYDREEMARMVACA
                                                                                                                                                                                                                                                                                                              KKFRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMGKIKRTGQGYSGPSL
                                                                                                                                                                                                                                                                                                                                                                593 IKFRKMALGTQEYGTGEYSNPTSDYGLYPSGSSSEQQATREMEMGKIKKTGQGYSGPSL
AAYYVPPPPSGFKAGGPYGGQQQYWQQQNASRPSDNHVVTSL-PPPKPPSPPPRAFPPPP
                         PPP-FMSSSGGSDYSDRPVLPPPSPGL/VLGFSKSTFTYEELARATNGFSFANLLGQGGFG
                                                                                                                                                                                     DFKFEAKVADFGLAKIASDINTHVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLE
                                                                                                                                                                                                                                                                                              AACVRHSARRPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDM
                                                                                                                               YEFVPNNNLELHLEGEGRPIMEMSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots, Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
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Prodom: PF000001; Buk_pkinase; 1.
PROSITE: PS00107; PROTEIN_KINASE_AIP: UNKNOWN_1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_SI; UNKNOWN_1.
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86.8%; Pred. No. 2.8e-182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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SEQUENCE 652 AA;
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| ret Local Similar
| 573; C
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01-JUN-2002
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Best Local (
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                                                                              15;
                                                                                                54 STPSAPPPSPPTPSTPGSPPDLPQPS--PPAPTTPGSPPAP--VEPPTRNPPPSVPGPPS 109
                                                                                                                                            NPSREGGSPRPPSSP-SPPSPSSDGLSTGVVVGIALGGVALLVIVT--LICLICKKKRRR 156
                                                                                                                                                        T-----TPSSPAAAAASSSGLTTPVVVGIVVGGLVVILLVILLVCLFKKKKRHH 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKAPSPPRQPPPPPPPPFMSSSGGSDYS----DRPVLPPPSPGLVLGFSKSTFTYEELAR
                                                                                                                                                                                                                                              CHPKIIHHDIKSANILLDARFEAKVADFGLAXLISDNNIHVSTRVMGTFGYLAPEYASSG
                                                                                                                                                                                                                                                                                                                                                                                                                        SSPSSPPPANOT ---ATPPPANOTAAPPPASNNSSSPPAPGSLSPPSLT-PPAAPSPPS
                                                                                                                                                                                       DEEDA------YY---VPPPPPPGPKAGGPYGGQQQQWRQQNATPPSDHVVTSLPPP
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                                                                                                                                                                                                                                                                           271 ATNGFSEANLLGOGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRH
                                                                                                                                                                                                                                                                                                                      LVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHED
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                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Somatic embryogenesis receptor kinase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-COLUMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                              55;
                                                       Length 597;
                                                                              Indels
                                3809FC29A222FEB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassicales; Brassicaceae; Arabidopsis
                                                       DB 10;
                                                  52.8%; Score low....
60.4%; Pred. No. 4e-110;
+ive 69; Mismatches 119;
 PS50311; PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 AA
PS50511; PROTEIN_KINASE_DOM;
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ETEMEMGSLKKDG 586
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                                64005
                                                                Best Local Similarity 50.49
Matches 370; Conservative
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                                 597 AA;
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                      Receptor; Kinase.
SEQUENCE 597 AA
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01-0CT-2000
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PROSITE;
           PROSITE;
                                                      Query Match
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185 GGPYGGQQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPFMSSSGGSD---- 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 YSDRPVLPPPSPGLVLGFS--KSTFTYBELARATNGFSEANLLGQGGFGTVHKGVLPSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical 66.7 kDa protein.
AT2G18470.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARWVACAAACVRHSARRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 HLAGKGRPTMEWSSRLKIAVGSAKGLSYLHENCNPKIIHRDIKASNILIDFKFEAKVADF
                                            Nakamura Y.;

Nakamura Y.;

Nakamura Y.;

Sequence features of Arabidopsis thaliana chromosome 3. II.

Facturinal analysis of Arabidopsis thaliana chromosome 3. II.

Sequence features of the regions of 4,251,695 bp covered by ninety P. TAC and BAC clones.";

DNA Res. 7.212.221(2000).

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

REMBL: AP000382; BAB02941.1;

R HSSP: P12931, IFMK.

InterPro: IPR004019; Euk_pkinase.

InterPro: IPR004040; STY_pkinase.

InterPro: IPR004040; STY_pkinase.

InterPro: IPR004040; STY_pkinase.

R Procom: P000001; Euk_pkinase. 1.

SMART; SM00221; STYKC; 1.

R PROSTIE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSTIE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSTIE; PS00108; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                    thaliana chromosome 3. II.
4,251,695 bp covered by ninety
                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
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DL-----YSNPISEYDLYPSWSSTDGQTTQGKATGNIKRPGQGY
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1769; DB 10;
Pred. No. 7e-107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 351; Conservative 34; Mismatches
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(TrEMBLrel. 10, Last sequ
(TrEMBLrel. 21, Last anno
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STRAIN=COLUMBIA;
MEDLINE=20363099; Pubmed=10907853;
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75.6%;
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1D 299
AC 299
DT 011
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DE HJ
ON AJ
OC BJ
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53.8 586

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288 NILGQGGFGYVHKGVLPSGKEVAVKSLKAGSGQGEREFQAEVDIISRVHHRYLVSLVGYC 347
                                                IAGAKRLIVYEFVPNNNLEIHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHR
                                                                         ---TP
                                                                                                                                           DIKASNILIDFKFEAKVADFGLAKIASDINTHVSTRVMGTFGYLAPFYAASGKLTEKSDV
                                                                                                                                                                                                                                     ESFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNGYDRE
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                                                                                                                                                                                                                                                                                                                                EMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSTGGSTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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-! - SIMILARIT: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NCV-1999 (TrEMBLrel. 12, Created)
01-NCV-1999 (TrEMBLrel. 12, Last sequence update)
01-NCV-1999 (TrEMBLrel. 20, Last sequence update)
Similar to somatic embryogenesis receptor-like kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            699 AA; 74329 MW; 97564B8A6389B0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             DSSQYNEDMKKFRKMALGTQEY --- NATGEYSNPISDYG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQTSYNADMKKFRQIALSSQEFPVSDCEGTSSNDSRDMG 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699 AA.
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InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002905; Ser_thr_pkinase.
InterPro; IPR004040; STY_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PR0011; PRCHEXTENSN.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
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Matches 372; Conserv
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                                                                                                         MEDIRE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Banstead M.B., Feldblyum T.V.,
Bueli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Salzberg S.L., Fraesc C.M., Venter J.C., White O., Eisen J.A.,
Salzberg S.L., Fraesc C.M., Venter J.C.,
Sequence, and analysis of chromosome 2 of the plant Arabidopsis
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Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Lan X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELOWGS IO THE SER/THR FAMILY OF PROTEIN KINASES.
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Hypothetical protein; ATP-binding; Serine/threonine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
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II; Brassicales; Brassicaceae; Arabidopsís.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.6%; Score 1748.5; DB 10; Best Local Similarity 56.8%; Pred. No. 2.3e-135; Matches 363; Conservative 78; Mismatches 151; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000719; Buk pkinase.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002905; Ser_thr_pkinase.
InterPro; IPR004040; Ser_thr_pkinase.
Pfan; PF00069; pkinase; 1.
PRINTS; PR01217; PRICHEXTENSN.
ProDon; PD00001; Euk_Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AC006135; AAD12219.1; -, EMBL; AC006439; AAM15257.1; -,
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                                                               FROM N.A.
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                     GSPPAAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSSPSPSPSSDGLSTGVVVGIAIGG 146
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ENSSDGSSSSSPPPPSDSSSQSQSPPP-PSTSPPQQSDNNGNKGNNENNKGNDGSSGDG 127
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                                                                                                                                                                                                                   LHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKITHRDIKASNILIDFKFEAKVAD
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                                    GNKNMSHTP----PPPSKTSDHSSHSOPRSLAPPTSNSGSNSSSNDGLANGGVIGLYAAA
                                                               VALLVIVILICIEC ---KKKRREDEEDAYYYPPPPPPGPKAGGPYGGQQQQWRQQNATPP
                                                                                                                                                        SD---RPVLPPPSPGLVLGFSKSTFTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
Gielen C., Van Montagu W., Hoheisel J., Jesse T., Heijnen L., Vos I.
Newes H.W., Mayer K.F.X, Schueller C., Bevan M.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.,
De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMG----KIKRTGQG 641
                                                                                                             SDHVVTSLPPPP----KAPSPPR----QPPPPPPFMSSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative serine/threenine protein kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TPPSPGANDDRNRTNGGNNNRDGSTPSPPSSGNRTSGDGGSPSPPRSISPPQNSGDSDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 GYVVGIAIGGVALLVIVILICLLCKKKRRRDEEDA----YYVPPPPPPPGPKA-GGPYGGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 QQQWRQQNATPPSDHVVTSLPPPFKAPSPPRQPPPPPPPPFWSSSGGSDYSDRPVLPPPS
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELOWGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
RM EMBL; AL023094; CAA18823.1; -.
RM EL, AL021094; CAA880161.1; -.
RM EL, AL021095; EUK_pkinase.
InterPro; IPR002209; Ser_thr_pkinase.
R InterPro; IPR004040; STY_pkinase.
R ProDOM: PD0000001; EUK_pkinase.
R PRODOM: PD000001; EUK_pkinase; 1.
SMART; SM00221; STKKC; 1.
RM PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
RM PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
RM PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
RM PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
RM PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
RM ATP-Dinding; Kinase; Serime/threonine-protein kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.9%; Score 1687; DB 10;
llarity 51.8%; Pred. No. 2.5e-101;
Conservative 87; Mismatches 142;
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Q9LS95;
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342 AKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIK
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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STRAIN-CV. COLUMBIA;
MEDLINE-21016719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REMEMGKIKRIG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EIRRGG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0T-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Somatic embryogenesis receptor kinase-ike protein.
Arabidopsis thallana (Mouse-ear cress).ike protein.
Bukaryota; Viridipplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosidae;
eurosids III Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSPSSD
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1 CALONES: 7.

1 CALONES: 7.

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3 CALONES: 7.

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7 CALONES: 7.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 48.0%; Score 1656.5; DB 10; Length 714; al Similarity 48.2%; Pred. No. 2.6e-59; 353; Conservative 80; Mismatches 146; Indels 153;
                                                                                                                                                                                                                                                                                                   Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 3. I features of the regions of 4,504,864 bp covered by sixty Pl
                                                                                                                                                                                                                                                                                              Kaneko T., Kato T., Asamizu E., Te
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         947338D8A8B4B250 CRC64;
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MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       714 AA; 76344 MW;
                                                                                                                                                                                                                                                               STRAIN-COLUMBIA;
Sato S., Nakamura Y.,
Submitted (APR-1999) t
                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura Y.;
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A Theologis A., Beker J.R., Palm C.J., Federspiel N.A., Kaul S.,
A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
A Buenler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
A Dunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujis C.Y.,
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A Gill J.E., Goldsmith A.D., Haas B., Hansen N.E., Hughes B., Huizar L.,
A Kim C.J., Con H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Leaz C.A., Li J.H., Li Y.-P.,
A Lin S.Y., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A Lin S.J., Ferson J., Pham P.K., Rizzo M., Rooney T., Rowiey D.,
Saxano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sax H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Wu D., Yu G., Fraser C.M., Wester J.C., Davis R.W.;
T. "Sequence and analysis of Chromosome I of the plant Arabidopsis
402 ASNILIDFKFEAKVADFGLAKIASDTNTHVSTRVMGTFG------YLAPEYAASGKL
                                                                         453 TEKSDVESFGVVLLELITGRRPVDANNVYVDDSLVDW-----ARPLENRASEQGDFESLA
                                                                                                                                                                                                      DAKMINGYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGIVSLSDLINEGMRPGQSN
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBirel. 17, Created)
01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-JUN-2002 (TrEMBirel. 21, Last annotation update)
Hypothetical 75.4 kDa protein.
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PRODOM; PNO00001; EUK_pkinase; 1.
SMART; SN00220; S_TKC; 1.
SMART; SN0019; TYRC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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                                                                                                            ** SAPPPTTPSSPPPPSTI 44
                                                                                                                          --STPGSP
                                                                                                                                                                                                                                  142 PPEQLPPPASSPQGGPKKPKKHHPGPATSPPAPSAPATSPGAPPNAPPRNSSHALPPKST
                                                                                                                                                                                                                                                                                                          KRRRDE--EDAXYVPPP--------PPPGPKAGGFTGGQQQQWRQQNATPPSDE
                                                                                                                                                                                                                                                                           202 AAGPLISPSR--GVPSSGNSVPPPANSGGGYQGKIMAGPALAGFAVIALMAVVFLVRRK
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Protein kinase-like protein.
Protein kinase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                     Gaps
                                                            DB 10; Length 710;
                                                                                    Indels 149;
                                     8B4420A8DD8F3AA6 CRC64;
                                                                                                                                                             ---SPPTP
                                                                                    158;
                                                                          Pred. No. 3.6e-90;
PS50011; PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_ST; 1.
ng; Hypothetical protein; Transferase.
7:10 Aa, 75371 MW, 884420AaDDER3AA6
                                                                                   81; Mismatches
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                                                            43.9%; Score 1515.5;
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                       ATP-binding;
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PROSITE;
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                                                                                                                                                                         3. II.
                                                                                                                                                                                                                                                                                                Fram: P000069; pkinase; 1.
Prodom: P000001; Euk_pkinase; 1.
SMART; SM00021; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM: 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
APP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 567 AA; 63160 MW; ECB5F6DEZ6855387 CRC64;
                                                                                                                                                     Nakamura Y.;

Nakamura Y.;

Structural analysis of Arabidopsis thaliana chromosome 3. II.

Sequence features of the regions of 4,251,695 bp covered by ninet
TAC and BAC clones.",

DNA Res. 7:217-221(2000).

-i SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; AB020746; BAB02005.1;

InterPro: IPR000719; BUA.pkinase.

InterPro: IPR004040; STL pkinase.

InterPro: IPR040404; STL pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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64.9%; Pred. No. 3.5e-90;
Live 37; Mismatches 38; Indels
                                                                     bato S., Nakamura Y., Asamizu E., To
to the EMBL/GenBank/DDBJ databases
 II; Brassicales; Brassicaceae; Arabidopsis
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Last sequence update)
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MEDLINE-20363099; PubMed=10907853;
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                                                                     Kaneko T., Kato T., 3
Submitted (DEC-1998)
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Best Local Similarity
                                        SEQUENCE FROM N.A.
                                                       STRAIN~COLUMBIA;
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01-MAY-2000 (
01-MAY-2000 (
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245 EILVPGSNNPSQNNPTLRPPLDAPNSTNNSGIGTGAVVGISVAVALVVFTLFGIFVWCLR 304  QY 251SPGLV	544 APEYASSGKLTEKSDVFSFGVVLJELITGRRPVDTSQPLGDESLVEMARPLISHALETEE 503 FEGLADAKANNGTDREEMARAVACAAACVRHSARRPPRASQIVRALEGNVSLSDLINGGRR 1:	STRAIN=CO MEDLINE=9 Sato S., Miyajima "Structur features Pl cloues Pl cloues [2] SEQUENCE Shinn P., Banh J., Hayashiza Karlin-Ne Miranda M Pham P.K. Tang C.C. Tang C.C. Tang C.C. Tang C.C. Shinn P.K. Tang C.C. Shinozaki "Arabidop Submitted [3] SEQUENCE Submitted [3]
01-MAR-2002 (TramBirrel. 20, Last ennotation update) F2445.8 protein (Hypothetical 75.1 kDa protein). Arabidopsis thaliana (Mouse-ear cress). Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBL_TaxID=3702; [1] SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA; Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S., Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H., Choi E., Chiou J., Altafi H., Aranjo R., Brooks S., Bechler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Howng B., Huizar L., Khan S., Kim C., Palm C., Pawler C., Pahler C., Pawler C., Pawler C., Pawler C., Pawler C., Pawler C., Phologis A., The sequence of BAC F2455 from Arabidopsis thallana chromosome 1."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. Yamada K., Liu B.X., Sakano H., Pham P.K., Banh J., Chung M.K., GoldSmith A.D., Tee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Indeer T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Schinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Full Length cDNA of gene F245.8 (G15734709); Submitted (MAY 2001) to the EMEL/GenBank/DBJ databases. I. SIMIARITY: BELOWS TO THE SER/THR FAMILY OF PROTEIN KINASES. EMBL: AC038076; AAA49974.1; - InterPro; IPR00296; ParloLextensn. InterPro; IPR00296; ParloLextensn. InterPro; IPR002096; ParloLextensn. InterPro; IPR00117; PRICHEXTENSN. InterPro; IPR00127; STYCC: 1. PR031TE: PS00107; PROTEIN_KINASE_DOM: 1. PR051TE: PS00108; PROTEIN_KINASE_DOM: 1. PR051TE: PS00108; PROTEIN_KINASE_ST; 1. ATP-binding: Hypothetical protein; Serine/threonine-protein Kinase; Transferase. SEQUENCE 708 AA; 75127 WW; AC0818E54B076328 CRC64;	Weith Match

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Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou | Seki M., Southwick A., Tang C.C., Ioriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581;
                                                                                              STRAILED CONTROLLES.

REASL, ABO05231. BAB10146.1;

REMBL, AR005231. BAB10146.1;

REMBL, AR005231. BAB10146.1;

REMBL, AR005681, AALTIGES.1;

REMBL, AR007681. PROMONING.

RICETPO: IPRO00388.1;

RICETPO: IPRO00388.2; Pistil_extensin.

RICETPO: IPRO02895. Pistil_extensin.

RICETPO: IPRO02895. Pistil_extensin.

RICETPO: IPRO02895. Pistil_extensin.

RICETPO: IPRO04040; STLEARINGS.

RICETPO: IPRO04245. TYLEARINGS.

RICETPO: IPRO04245. TYLEXIENSE.

REMARY: PRO1217. PRICEXIENSIN.

REMARY: SMO0221; STRKC; 1.

SMARY: SMO0221; STRKC; 1.

REMARY: SMO0221; STRKC; 1.
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PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 681 AA; 72389 MW; F64DAA1E470E73F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.2%; Score 1456; DB 10;
46.4%; Pred. No. 2.5e-86;
iive 87; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Arabidopsis cDNA clones.";
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READLINE—21016719; PubMed—11130712;

RA THOLOGIS A., ECKET J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White D., Elably M. T.V., Chen H., Cheuk R.F., Chin C.W.,

RA Gill J.E., Goldsmith A.D., Rass B., Ransen M.F., Huizer L.,

RA Gill J.E., Goldsmith A.D., Rass B., Ransen M.F., Huizer L.,

RA HINTER J.L., Kreenenetskaia I., Kurtz D.B., Kan B.,

RA Langin-Hooper S., Lee A., Lee J.W., Leiz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nayen M., Naerman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Win B., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

**Restance and analysis of chromosome I of the plant Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
-FDSRQQSAQIRMEQRMAFGSQDESS
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PROSITE: PSSO011; PROTEIN KINASE DOM; 1.
PROSITE: PSO0108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 760 AA; 80713 MW; 758 BEFLF37C742D7 CRC64;
                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pto Kinase interactor, putative.
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Pred. No. 7.6e-85;
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EMBL; AC079829; AA550687 1; -
InterPro: IPR00219; Buk_pkinase.
InterPro: IPR002296; P_rich_extensn.
InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR01217; PRICHEXIENSN.
PRODOM: PD00001; Buk_pkinase; 1.
SMART: SM00220; S_TKC; 1.
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45.9%;
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Best Local Similarity 45.9
Matches 313; Conservative
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ID 03
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            SPRKSYSCEDNP-SPNNPTPVIDNSSSGISIAAVVGVSIG--YALVLITLIGVVVCCL 352
                                                                                                                                                       SNPSREGGSPRPPSSPSPPSP----SSDGLSTGVVVGIAIGGVALLVIVILI----CLL 159
                                                                                                                                        LLGQGGFGYVHKGYLPSGKEVAVKQLKYGSGQGEREFQAEVEIISRVHHRHLVSLVGYCI 339
                                                                                                                                                                                       AGAKRILVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKITHRD 399
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                                                         IKASNILIDFKFEAKVADFGLAKIASDTNTHVSTRVMGTFGYLAPEYAASGKLTEKSDVF
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                                                                                         PPROPPPPPPPPPPMSSSGGSDTSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEAN
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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA:
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
Li J., Kremenetskala I., Luros J., Altafi H., Gonzalez A., Araujo R.,
Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L.,
Kim C., Palm C.J., Rowley D., Shinn P., Kalker M., Davis R.W.,
Ecker J.R., Federspiel N.A., Theologis A.;
*Arabidopsis thaliana chromosome I BAC F508 sequence.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Theologis A.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AC005990; AAC98010.1; -.
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Last annotation update)
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InterPro; IPR002965; P_Tich_extensn.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; I.
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SAQQSAEIRLFRRMAFGSQNYS 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 PSDHVVTSLPPPPKAPSPPRQPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKST
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                                                                                                                                                                           ---APPTTPSSPPP
                                                                                                                                                                                                                                        41 PSTIPTSPPPSSRSTPSAP----PPSPPTPSTPGSPPP-----LPQPSPPA----PTTP
                                                                                                                                                                                                                                                                                                                          ----SSDGLSTG-----WWGIAIGGVALLVIVILICLL
                                                                                                                                             Gaps
                                                                                                                                           Indels 169;
                                                                                                             Length 731;
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                                                                Transferase
Prodom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Serine/threonine-protein kinase; Transfer; SEQUENCE 731 AA; 77639 MW; 45D93AD5C450001B CRC64;
                                                                                                             DB 10;
                                                                                                                                           156;
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                                                                                                                            ; Pred. No. 1.1e
93; Mismatches
                                                                                                            Score 1415.5;
Pred. No. 1.16
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                                                                                                                            43.48;
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Best Local Similarity
Watches 321; Conser'
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